

Sequence Listing



<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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gtgggtgtcac cgattataga gattggacag atactaatta ttactcagaa 550

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Leu Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val	50	55	60
Pro Phe Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly	65	70	75
Thr Phe Gly Cys Phe Ala Thr Cys Arg Ala Ser Ala Trp Met Leu	80	85	90
Lys Leu Tyr Ala Met Phe Leu Thr Leu Val Phe Leu Val Glu Leu	95	100	105
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Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35					40					45

Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50					55					60

Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65					70					75

Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120

Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125					130					135

Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195

Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	
	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	
	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	
	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	
	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	
	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	
	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	
	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	
	305	310	315

Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gcccttggg ccgtcgccac cactgtagtc atgtaccac ccgcgcgcgc 150
 gccgctcat cggaacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggtaaaac cagcaaatac accgctctta ccagctctc agaaggcgga 450
 caccgacct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
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 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgacga 900
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 aacctgctca gctggacgc ctacgtgttc aacaccgaag cccacctct 2100

gctatctgg accctgcct aggggtgatg gctgctggtg tggggaacttc 2150
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 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
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 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asn	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe			

	395		400		405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu Ala			
	410	415			420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys Lys			
	425	430			435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu Phe			
	440	445			450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser Tyr			
	455	460			465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln Glu			
	470	475			480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val Arg			
	485	490			495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe Val			
	500	505			510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His Leu			
	515	520			525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His Gly			
	530	535			540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu Thr			
	545	550			555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro Glu			
	560	565			570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp Val			
	575	580			585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro Glu Thr			
	590	595			600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg Lys			
	605	610			615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg Phe			
	620	625			630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val Gln			
	635	640			645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe Phe			
	650	655			660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp Asp			
	665	670			675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu Ala			
	680	685			690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttgccctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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ccctcggaag tgttcgtct tccacctgtt cgtggcctgc ctctcgtctg 200
gtttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

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cm magtca ggggacaagg gcaggagacc tggggccctc cccgtgectg 300
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ctgggtcttg tgccccacat ggcgcgcttc ctgagcagga agaagatccg 450
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aaaaaaaaa aaaaaaaaaa aaaa 1524

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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
<220>

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<219> sig_peptide
 1-42
 Signal peptide.

<220> misc_feature
 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
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 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Asn Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp	
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Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu	Ala	
170	175	180
Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
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<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
atggtgctggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<210>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttctctgagc aggaagaaga tccggcaccg catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggctcg tgcacagaaa gtctctctctg ccactgacgc ccccatcagg 150
gattggggcct tctttccccc ttcctttctg tgtctctctg ctcatcgggc 200
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<225> Growth factor and cytokines receptors family.

<400> 22

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Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
          20             25             30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
          35             40             45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
          50             55             60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccgcggc 150
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cccggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250
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gtggatgcac cgtcgggtaa aggagaagaa catcacgga cgggatacca 850
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 tgatgaacgt gtctgtggc tgggcagag ggaagctaaa gcctgcagta 1750
 ggattgtgca gtgtcttcag cgcattgcta cctaccggct agccgggtga 1800
 gctcactgtt attcaacata ttaccccaat attgctctgg aaqcttatgt 1850
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900
 tggcagctc tgatcgtaca ggactttcgg attatggga gcyggatcca 1950
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 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gaatttcaag 2200
 ggccctagc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat ttataactg cagtgggala aatgcaata tactattgtt 2300

atgtgaaa aaattttatt tgacttaaaa gtittattat ttgttttttt 2350
 gctcttgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
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 ctaatggaac cacatttttt tcaacttagct ttctgtgggc atgtgtaatt 2700
 gtattctctg cggtttttaa tctcacagta ctttatttct gtcttgccc 2750
 tcaataatat cacaacaat attccagtc ttttaattggc tgcataataa 2800
 ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type 11).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

380	385	390	
Glu Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe	395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val	410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr	425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu	440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu	455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys	470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu	485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala	500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg	515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile	530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met	545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly	560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys	575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu	590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr	605	610	615

Ser

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggtt eggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtaacgggat accaggtgtg ttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctgggtgtg 50
ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagAAC agattatTTT gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtage ttagtagtat ctccatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtecccttat atctgaataa aggagtgtgg gcagacactt 450
tttgaagag tctgtctggg tgatcctggg agaagcccca ttagggtcac 500
tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgac agtcggcatg 600
 atgacgaagc cacgagaaca tccacctcag aaggactgga ggaaggtgaa 650
 gtggagggag agacgtctct gatcgtcgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu
 1 5 10 15
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
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 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100
 tccgtggatt cctctgctaa gaccgtgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttggggcctg ggggtcccca 200
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250
 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtcgg tggctagcgt 300
 gggcgcttgg acgggggtcca tgggcaactg gtccatgttc acctgggtgt 350
 tctgtttctc cgtgacctg atcattctca tctgtggagct gtgcgggctc 400
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ctatggggcc ctcttctgcc tctgggctc cctcatctac cccaccacct 500
 atgtccagtt cctgtccac ggcgttgc gggaccacgc cctgcgcgc 550
 acctctttct cctgcctgc gtgtgtggt tacgccaccg aagtggcctg 600
 gaccggggcc cggccggcg agatcactgg ctatatggcc accgtaccgc 650
 ggcctgtgaa ggtgtggag accttcgtg cctgcctcat ctgcgcctc 700
 atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtggt 750
 ggcggtgtac gccatctgct tcctcctagc ggccatcgcc atctgtctga 800
 acctggggga gtgcaccaac gtgctacca tcccttccc cagcttctc 850
 tgggggtgg ccttctgtc tgcctctc tatgccaccg ccttcttct 900
 ctggccctc taccagtgc atgagaagta tggcgccag cctgcgcct 950
 cgagagatgt aagctgcgc cgcagccatg cctactacgt gtgtgcctgg 1000
 gaccgcgcac tggctgtgc cctcctgac gccatcaacc tactggcgta 1050
 tgtggtgac ctggtgcact ctgccacct ggttttctc aaggtctaa 1100
 actctccaa gaggtcccg tccctctcc aacctcttg ttctcttgc 1150
 ccgagtctt tttatggagt acttcttcc tccgccttc ctctgttct 1200
 ctctctctgt ctccctccc tccacctt ttcttctct cccaattct 1250
 tgcactctaa ccagtcttg gatgcactt ctctctccc ttctctctg 1300
 ctgttctct cctgtgtgt tttgttgc acatctgtt ttcacctg 1350
 agctgttct cttttcttt tcttcttt tttttttt ttttaagac 1400
 gattctact ctgtggcca ggtggagtg cagtgggtgc atctcagct 1450
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attaaaaaac atatataat atatatttgg aggtcagtaa ttccaatgg 1950
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000
 cagccttgcc agagattggc tccagaatct ttgccaggct tacagaacac 2050
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
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 20 25 30
 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
				305					310					315	
His	Leu	Val	Phe	Val	Lys	Val									
				320											

<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

<400> 32
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 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200
 taaacattgg gcactacagt gacccaaaca gactgaattc cccaagagcc 250
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300
 ttattactca ctatgactaa gggtcacaaa tggggtagct tgatggagag 350
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 aggaaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450
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 aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggaactt 650
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 . tgggtgtg ggggttttgt ttccatcttg ccgagtctgc cggaatgtgg 850
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 gcccaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600

ggttcattag gtgtttattt tgttctattt aagaatttgt tttattaaat 3650

taatatataaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
1				5					10					15

Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
			20						25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
			35						40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
			50						55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
			65						70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
			80						85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
			95						100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
			110						115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
			125						130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
			140						145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
			155						160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
			170						175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
			185						190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
			200						205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
			215						220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
			230						235					240

Ala Ser Gln Leu	Leu Gly Asp Glu Leu	Leu Leu Ala Lys Leu	Pro
245	250		255
Pro Ser Arg Glu	Ser Ala Phe Arg Ser	Leu Gly Pro Leu	Glu Ala
260	265		270
Gln Asp Ser Leu	Tyr Asn Ser Pro Leu	Thr Glu Ser Cys Leu	Ser
275	280		285
Pro Ala Glu Glu	Glu Pro Ala Pro Cys	Lys Asp Cys Gln Pro	Leu
290	295		300
Cys Pro Pro Leu	Thr Gly Ser Trp Glu	Arg Gln Arg Gln Ala	Ser
305	310		315
Asp Leu Ala Ser	Ser Gly Val Val Ser	Leu Asp Glu Asp Glu	Ala
320	325		330
Glu Pro Glu Glu	Gln		
335			

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct

<400> 34
 tgtcctttgt cccagacttc tgtcc 25

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 35
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 36

ttccactcaa tgagggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggg cgctctgtta cacaagcaag atacagccag cccacctaa 50

ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100

ccatctgttt tctetaatgc acgacagatt cctttcagac aggacaactg 150

tgataatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

tactagccat tgtgagcttc agttttcttca tctgcaaaat gggcataata 250

caatctattc ttgccacatc aagggtattgt tattccttta aaaaaaac 300

aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
 caatgttgtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
 caataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
 ttttctatt tttttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
 atataccac ctcaaatctc aaggcgagtc attccccctc tttgaacta 550
 ctcaataaca gccacggaat aacagatttc tccagtaact catcagcaga 600
 ctattttttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650
 ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
 gatgaagatc ttttgcccat ctacgcacat cccaatgcta cacctgctct 750
 gtcttcagaa aacttcactt ggtcttttgt caatgacacc gtgaaaactc 800
 ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
 ccatctgtga cccctttgat agtggaaacca agtggatggc ttaccacaaa 900
 cagtgatagc ttcaactgggt ttacccttta tcaagaaaaa acaactctac 950
 agcctacett aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
 gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050
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 gtgaaaaaag gaaaacggat tcattttccc atcgggcact ttatgacgac 1150
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 gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250
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 cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350
 gcaagtgtca tctacatcct agccttttga caaattcctc tttcaaaagg 1400
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 aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500
 tttcttaca tttttggcca tctgaggca tttactaagt agccttaatt 1550
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 tgccatgaagc cctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750

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 ...ag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850
 ...ile tagtacgtta taattttcta gatcagcaca cacatgatca 1900
 ...tgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
 ...agctg accctaccda ggaaagtaat agcttcttta aaagtcttca 2000
 ...tttgg gaattttaa tigtcttaat ataicttagg ctccaattat 2050
 ...tgcctgact taaaaactca atgagaatca tggc 2084

<210> 41
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
 1 5 10 15
 Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
 20 25 30
 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
 35 40 45
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105
 Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
 110 115 120
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
 125 130 135
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
 140 145 150
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
 155 160 165
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
 170 175 180
 Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
 185 190 195

Arg	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Glu	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Glu	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcctgcag tctgcagccc aggaacgtga ttccagcagc 50
 gccttaccgc gcagcccga gattcactat ggtgaaaatc gccttcaata 100
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccaccacg gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccaa gacaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
 tcttgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

gaaatgata tctgatgccc ctcaataactt ctattgttat gctccaaaa 600
 aactctggtag agctcttttg caaactggcg agtggcagat atctgctca 650
 aatttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtgatg 700
 tttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtc 750
 ttccgcttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800
 tgataaatgc tggagatta gacactccc caacgaattt attgttgaga 850
 ccaagatctg tcaagagtaa gaggcacag atagagtgtc ctgggtaata 900
 agaagtcaga gatttacaat atgactttaa cattaagggtt tatgggatac 950
 tcaagatatt tactcatgca ttactctat tgcctatgct ttaaaaaaag 1000
 gaaaaaaaaa aaactacta accactgcaa gctcttgica aattttagtt 1050
 taattggcat tgcctgtttt ttgaaactga aattacatga gtttcatttt 1100
 ttcttgcac ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
 tttttctttt ccttlaagta agctctttat tcatcttaig gtggagcaat 1250
 tttaaaattt gaaatatattt aaattgtttt tgaacttttt gtgtaaaata 1300
 tatcagatct caacattgtt ggtttctttt gtttttcati ttgtacaact 1350
 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgcctctgtaa 1400
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
 tgtgtagggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550
 cctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
 1 5 10 15
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
 20 25 30
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
 35 40 45
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr		
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<210> 20
<211> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgcaqtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgagqcaq 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggggggcag ygcgcagccc agagcagccc cgggcaccaq 50

mmpactet ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100
 cgggagcacc cagtcctgta cggcaaggaa ctggctcctgg gggcaccatg 150
 ctcttggcgg cagcccccag cctcctcacc ctctctgttg tgetgctggg 200
 gtctgtgect gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
 tggaggaatgt ggcgggtagt ggggagggcg agggctcgtc ggctcctcc 300
 ccgagcctcc cggcaccctg gaccccggcc ctacgcccc aatcgatggg 350
 gcccagcccc acaaccctgg ggggccctc accccccacc aacttctgg 400
 atgggatagt ggaattcttc cggcagtaag tgatgctgat tgetgtggg 450
 ggtcccttgg cctttctgt gatgttctc gtctgtgccc cgtctctac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgtcc tccccaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag cctggattc 650
 ctcccgccag ctccaggccg acatcttggc cggcaccag aacctcaagt 700
 cccccaccag ggttgcactg ggcgggtggg acggagccag gatggtggag 750
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
 agtccaggga catggggctc cagtggagac accagaggcg caggaggagc 850
 cgtgctcagg ggtccttgag ggggctgtg tggccggtga gggccaaggg 900
 gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
 tccccccgaa agcccctgtg ctctgcagcag tgctccccc agtgtctaac 1000
 agtccctccc ggttgccagc cctgactgtc gggcccccaa gtggtcacct 1050
 cccgtgtat gaaaaggcct tcagccctga ctgcttctg acactcctc 1100
 cttggcctcc ctgtgggtgc aatcccagca tgtgtgatt ctacagcagg 1150
 cagaaatgct ggtccccggt gccccggagg aatcttacca agtgccatca 1200
 tcttccact cagcagcccc aaagggtac atctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
 tacttlttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgtc ttaattttcc tgaagggtgc cccctgttct tagttggctc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

cccaccccc cggcctgggg gtgagtttct cctcccgcga ctgctgctgg 1550
 gatcaggttg aatgaatgga actcttctctg tctggcctcc aaagcagcct 1600
 ggaagctgag gggctgtgtt tgaggggacc tccacctgg ggaagtcga 1650
 gggctgggg aagggtttct gacgccccagc ctggagcagg ggggcctgg 1700
 cccccctg ttgtcacac attgtctggc agcctgtgtc cacaatatte 1750
 gtcagtcctc gacagggagc ctgggctccg tctgtcttta gggaggtct 1800
 ggraggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260	265	270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val	275	280	

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggtgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgtctgg cctctgcct gggcagtcgg gaggtggcc 250
 cctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggcattgg 350
 caaagaggcc ggaggggcag ctggtctctaa agtcagttag gcccttggcc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaagggtg 650
 ccttgaggcc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtgg gcagcagtgg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagt gcggcagcag tggcggcagc 1050
 agtggtgga gcagtggcaa cagtgggtgg agcagaggtg acagcggcag 1100
 tgagtctctc tggggatcca gcaccggctc ctctctcggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200
 gaagcccggg ggagcgggga atctgggatt cagggettca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300
 gaggtcttgg agacaattat cgggggcaag ggtcagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcctc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag ccccccacact 1550
 ccttccttaa aacaccaccc tctcatcact aatctcagcc ctctgccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr	65	70 75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly	80	85 90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala	95	100 105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val	110	115 120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val	125	130 135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile	140	145 150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro	155	160 165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser	170	175 180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln	185	190 195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly	200	205 210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln	215	220 225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly	230	235 240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser	245	250 255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly	260	265 270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser	275	280 285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser	290	295 300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310 315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	325 330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335	340 345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
 350 355 360
 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
 365 370 375
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
 380 385 390
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
 395 400 405
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
 410 415 420
 Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
 425 430 435
 Ser Ser Arg Ile Pro
 440

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaccggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggctg 50
 caggcccggc gggcggtgct caccgtgccc tggtcgttg aqtttctctc 100
 ctttgcctgac catgttgttc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagttag 200
 gggaagatgt gtttcccgaa caagctgctg ctacttgctg tccctgggctg 250
 gcttttccag attcccacag tccctgagga cttgttcttt ctggaagagg 300
 gtccctcata tgccttigag gtggacacag tagccccaga gcatggcttg 350
 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
 catcggagag ctccggaaac tgctcgttcc gtgggtgtca ggcagtagtg 450
 gacggagtgg gggttccatg aggaaaatca cccccaccac taccaccagc 500
 ctgggagccc agccttccca gaccagccag gggtgcagg cacagctcgc 550
 ccaggccttt ttccacaacc agccgccttc cttgcgcggg accgtagagt 600
 tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650
 ctggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700
 ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750
 tgtgttccca gctgtgcctt caccggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccttggggt glgcgggcgc tcttccaga 850
 ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900
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670 FRT
671 Homo sapiens

400 58

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Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
				185					190					195
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
				200					205					210
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
				215					220					225
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
				230					235					240
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
				245					250					255
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
				260					265					270

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly Arg			

	560		565		570
Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln			
	575		580		585
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp			
	590		595		600
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile			
	605		610		615
Per Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg			
	620		625		630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys			
	635		640		645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile			
	650		655		660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly			
	665		670		675
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu			
	680		685		690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr			
	695		700		705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr			
	710		715		720
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met			
	725		730		735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr			
	740		745		750
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys			
	755		760		765
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His			
	770		775		780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn			
	785		790		795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr			
	800		805		810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro			
	815		820		825
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg			
	830		835		840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro			
	845		850		855

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu		950	955	960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His		965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly		980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro		995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys		1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg		1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro		1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu		1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp		1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly		1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr		1100	1105	1110
Pro	Pro	Leu	Thr	Ile												1115		

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<210> Artificial sequence
<211> 1-25
<213> Synthetic construct.

<400> 59
cttctacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gagg 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccocaaag ccacaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgaggaggctg ggtcgtcattg atccggaccc cattgtcggc ctctgcccat 50
cgctgtctcc tccagggctc ccggggccga ccccgccga acatgcagcc 100
cacggggccgc gaggggtccc ggcgcctcag ccggcggtat ctgcggcgctc 150
tgctgtcctt gctactgttg ctgtgtctgc ggcagcccggt aaccgcgcgcg 200
gagaccacgc cggggcgcgc cagagccctc tccacgttgg gctcccccag 250
cctcttcacc acgcggggtg tcccagcgc cctcactacc ccaggcctca 300
ctacgccagg caccocccaaa accctggacc ttgggggtcg cgcgcagggc 350

ctgatgggga gtttcccact cgtggacggc cacaatgacc tgcgccaggt 400
 cctgagacag cgttacaaga atgtgcttca ggatgttacc ctgcgaaatt 450
 tcagccatgg tcagaccagc ctggacaggc tttagagacgg cctcgtgggt 500
 gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
 cgtgcgcctc gccctggagc agattgacct cattcacgcg atgtgtgct 600
 cctactctga actcgagctt gtgacctcag ctgaaggctc gaacagctct 650
 caaaagctgg cctgcctcat tggcgtgnag ggtgggcact cactggacag 700
 cagcctctct gtgtgcgca gtttctatgt gctgggggtg cgtacctga 750
 cacttacctt cacctgcagt acaccatggg cagagagttc caccagttc 800
 agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850
 agtagtagag gagttgaacc gctgggcct gatgatagat ttgtctatg 900
 catcggacac cttgataaga agggctctgg aagtgtctca ggctcctgtg 950
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cgggggcctc ctgatggtga 1050
 cactgtccat gggggtgctg cagtgcaccc tgccttgctaa cgtgtccact 1100
 gtggcagatc actttagcca catcagggca gtcattggat ctgagttcat 1150
 cgggattggg ggaaattatg acgggactgg ccgggttccct caggggctgg 1200
 aggatgtgtc cacataccca gtctgatac aggagttgct gactcgtasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaaacc tctgcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggaggtga gtttccatat gggcaactga gcacatcctg ccactccac 1400
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaccaat cgggtccctt ggaggtcctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tctgacaca gtcggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tcttgagaat aaacatgta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>

<21> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
1				5					10					15	
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatcccteta tgaactgcaat gtgaggtgtc cggcttltgt 100
ggcccagcaa gcttgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgca gtgcctggcc atgacgtgga ggccactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtggg tgcctgtgtg ctctacatgg ccttctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650
 atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctaact 750
 ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
 ctcttctcc ctaacttlag aaatgttgta cttggctatt ttgattaggg 850
 aagagggatg tggctctga tctctgttgt cttcttgggt ctttggggtt 900
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
 ctcaggagtg gatgcgatct gtctctctctg gctccactct tgccgccttc 1000
 cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050
 ttcaggaaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
 gttcctttct gcagtgggtc ttatcaccac ctccctccca gcccgggcgc 1150
 ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200
 tgggccccct gagcccactg ggtcttcagg gtgcactgga agctggtgtt 1250
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 ctctgctgcc ggtccctcca cctgcacttg aggggtctgg gcagtccctc 1350
 ctctccccag tgtccacagt caetgagcca gacggctcgt tggaaacatga 1400
 gactcgaggc tgagcgtgga tctgaacacc acagcccttg tacttgggtt 1450
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tctcttgctc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 tttattttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	65	70	75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	80	85	90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	95	100	105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	110	115	120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	125	130	135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	140	145	150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	155	160	165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	170	175	180

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
 agttcatagg gtcttggttc cccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtectccc 150
 tccctttgca tccccacccc tccgggcttt gcgtcttctt ggggaccccc 200
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
 tgctctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggcca aactcaactc catcaagtec tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagteccc accaaggatc 500
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
 gcatgtgctg ccccgatacc cgtgcaata atggcatctg tatccagtt 600
 actgaaagca tcttaacccc tcacatccc gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccattgacttg ggaatggcaga 700
 atcttaggaag accacacact aagatgtcac atataaaagg gcatgaaggga 750
 gaccctctgcc tacgatcacc agactgcatt gaagggtttt gctgtgctcg 800
 tcattttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
 gtaccaaaca acgcaagaag ggttctcatg ggettgaaat ttccagcgt 900
 tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccacctt 950
 ctctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
 ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
 catggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100
 gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
 aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
 caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250
 agagaacaag cacacagtgg aaattactga tgagttagcat gtgactttcc 1300
 aagagttag gttgtgctgg aggagaggtt tcttcagat tgcgtattgc 1350
 ttatacaaat aacctacatg ccagatttct attcaacgtt agagttaaac 1400
 aaaatactcc tagaataact tgttatataa taggttctaa aaataaaatt 1450
 gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
 taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttgg 1550
 agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
 cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
 ccacaaatac tttttttcca aaattttagt ttacctgta attaataaga 1700
 actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
 atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800
 aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850
 ttccagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900
 gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950
 gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000
 agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
 aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt ttggtgttca tttttgaaac caggggatgc acagtctaaa 2150
 tgaatatctg catgggattt gctatcataa tttttactat gcagatgaat 2200
 tcaagtgtgag gtctgtgtc cgtactatcc tcaaattatt tailltatag 2250
 ttgtgagatc ctcaaataat ctcaatttca ggaggtttca caaaatgtac 2300
 tcttgaagta gacagagtag tgaggtttca ttgcccctca taagcttctg 2350
 actagccaat ggcacatcc aattttcttc ccaaacctct gcagcatctg 2400
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 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
 gcagaatata ttgacagcta ttgactttgt aatttaggaa aaatgtataa 3100
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 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25				30	

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40				45	

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 acatcacgtt tttaaaaatt gattttctca aattcatggc aaatatttcc 150
 ctcccttcta actttctatg tcagaatgag gaaggatagc tqcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
 atattttagt aattcatatg ttttagatta taggttttaa catacttggtg 300
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 ggatttggtt ttttatcccc cttttaaagt catccgtcct tggttcagga 400
 ttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
 ttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
 ctcaagcccc caacatcccc gtctcagtc ctccagtcac ttgacttcaa 600
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 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
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 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
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 ccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
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 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

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 gccggggtgtg gtggcggggc gtgcctgtaa tcccagctac ttgggagggt 1750
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 ctg taaqa 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72
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 20 25 30
 Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
 35 40 45
 Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
 50 55 60
 Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
 65 70 75
 Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
 80 85 90
 Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
 95 100 105
 Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
 110 115 120
 Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
 125 130 135
 Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
 140 145 150
 Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
 155 160 165
 Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 170 175 180
 Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
 185 190 195
 Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
 200 205 210
 Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 215 220 225

Val	Leu	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Leu	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
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<210> 75
 <211> 50

<21> RNA
<211> Artificial

<212> Artificial sequence

<213> 1-50

<214> Synthetic construct

<40> 75

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<21> 76

<211> 1989

<212> DNA

<213> Homo sapiens

<400> 76

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tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
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 ccactctcag cccccacat ttgcctctgc tgggtggacct gccaccatca 1950
 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30

Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45

Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60

Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

2000 - 78

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 gccattgggt caagggcgta ataaatactt gctatttcaa aaa 2243

<210> 79
 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 79
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 Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
 20 25 30
 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
 35 40 45
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
 50 55 60
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
 65 70 75
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
 80 85 90
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
 95 100 105

Val	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	
				110					115					120	
Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val		
			125					130					135		
Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr		
			140					145					150		
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	
			155						160					165	
Arg	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	
			170						175					180	
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	
			185						190					195	
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	
			200						205					210	
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	
			215						220					225	
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	
			230						235					240	
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	
			245						250					255	
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	
			260						265					270	
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	
			275						280					285	
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	
			290						295					300	
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	
			305						310					315	
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	
			320						325					330	
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	
			335						340					345	
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	
			350						355					360	
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	
			365						370					375	
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	
			380						385					390	
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys	

395	400	405
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410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
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<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

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<210> 83
 <211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

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<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro	Glu
170	175	180	
Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu	Lys
185	190	195	
Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200	205	210	
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215	220	225	
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230	235	240	
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245	250	255	
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260	265	270	
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275	280	285	
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290	295	300	
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305	310	315	
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320	325	330	
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335	340	345	
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350	355	360	
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365	370	375	
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380	385	390	
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395	400	405	
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410	415	420	
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425	430	435	
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440	445	450	
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
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Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
	560		565		

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 <211> 3316
 <212> DNA
 <213> Homo sapiens

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 cttctcagat gccaaagacta tgtatgaggt ttccaaaga ggactcgtctg 500
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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			20						25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	
				35					40					45	
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	
				50					55					60	
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	
				65					70					75	
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	
				80					85					90	
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	
				95					100					105	
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	
				110					115					120	
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	
				125					130					135	
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	
				140					145					150	
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	
				155					160					165	
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	
				170					175					180	
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	
				185					190					195	
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	
				200					205					210	
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	
				215					220					225	
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	
				230					235					240	
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	
				245					250					255	
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	
				260					265					270	
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	
				275					280					285	
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	
				290					295					300	
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	
				305					310					315	
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr	

	320		325		330
His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys	Val		
	335		340		345
Glu His Ala Tyr	Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser	Tyr		
	350		355		360
Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val	Val		
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
	380		385		390
Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys	Gly Ile Ile Arg His	Asp		
	440		445		450
Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
	455		460		465
Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
	470		475		480
Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
	485		490		495
Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
	530		535		540
Phe Thr Val Asn	Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr	Asn		
	545		550		555
Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
	560		565		570
Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		
	605		610		615

Asp	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Glu	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
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 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu	Asn	Gln	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Asp	
				140					145					150	
Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn	
				155					160					165	
Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Cys	Thr	Val	Lys	Asp	Glu	
				170					175					180	
Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser	
				185					190					195	
Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp	
				200					205					210	
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His	
				215					220					225	
Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu	
				230					235					240	
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	
				245					250					255	
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser	
				260					265					270	
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr	
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Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu	
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Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn	Tyr	Leu	
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Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro	
				320					325					330	
Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met	
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Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro	
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Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys	Ala	Ser	
				365					370					375	
Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe	Ala	Val	
				380					385					390	
Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	
				395					400					405	
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr	
				410					415					420	
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	

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Asp Pro Ala Leu	Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu	Gly		
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Trp Val Leu Arg	Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro	Lys		
	455		460		465
Trp Pro Thr Pro	Glu Lys Leu Trp Asp	Trp Asp Met Trp Met	Arg		
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Met Pro Glu Gln	Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp	Val		
	485		490		495
Ser Arg Ser Tyr	His Phe Gly Ile Val	Gly Leu Asn Met Asn	Gly		
	500		505		510
Tyr Phe His Glu	Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr	Val		
	515		520		525
Pro Gly Val Gln	Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu	Ala		
	530		535		540
Tyr Glu Val Glu	Val His Arg Leu Leu	Ser Glu Ala Glu Val	Leu		
	545		550		555
Asp His Ser Lys	Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp	Thr		
	560		565		570
Glu Gly His Thr	Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp	Asp		
	575		580		585
Asp Phe Thr Thr	Trp Thr Gln Leu Ala	Lys Cys Leu His Ile	Trp		
	590		595		600
Asp Leu Asp Val	Arg Gly Asn His Arg	Gly Leu Trp Arg Leu	Phe		
	605		610		615
Arg Lys Lys Asn	His Phe Leu Val Val	Gly Val Pro Ala Ser	Pro		
	620		625		630
Tyr Ser Val Lys	Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu	Glu		
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Pro Pro Pro Lys	Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln	Thr		
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<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

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 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 90
 cctcaaccag gccacgggcc ac 22

 <210> 91
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-24
 <223> Synthetic construct.

 <400> 91
 cccaggcaga gatgcagtac aggc 24

 <210> 92
 <211> 26
 <212> DNA
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 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 92
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 <210> 93
 <211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 93
 ctcacctcat gaggatgagg ccattgtgct attcctcaac atggtag 47

 <210> 94
 <211> 3037
 <212> DNA
 <213> Homo sapiens

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<211> 95
<212> 307
<213> PRT
<213> Homo sapiens

<210> 95
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35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
95 100 105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240
Leu	Ala	Thr	Gly	Val	Ala
	245	Met	Leu	Phe	Ser
					250
					255
Val	Ala	Thr	Val	His	Val
	260				265
					270
His	Ser	His	Lys	Pro	Asp
	275	Ala	Thr	Gly	Gly
					280
					285
Leu	Glu	Val	Ala	Ala	Leu
	290	Val	Leu	Gly	Cys
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					300
Leu	Ser	Val	Gly	His	Gln
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<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gtccatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
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<210> 99
 <211> 1429

<212> DNA
<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr	245	250	255
Asn	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu	260	265	270
Pro	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val	275	280	285
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro	290	295	300
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met	305	310	315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu	320	325	330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu	335	340	345
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser	350	355	360
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile	365	370	375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu	380	385	390
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<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 ctggcatctc agtgggcaat atccccaggc ttccattct gccctctact 1450
 cctgacacct gtggcctggg gcctgggttg ggccatagcg tatgtggac 1500
 tctgggaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550
 gctgcagtga gctcattcct ccttttctg tggaaagcct gggctggctg 1600
 ggggtccaag agggccctgg caaccctggt tcccatccct gggeccgtcc 1650
 tgttactcct gctgttctgc ttggctgtgt tcttctctga tagttttgtt 1700
 gtagctgagg ccagggccac ccccttctt ttgggctcat tcatectgct 1750
 cctggttgtc cagcttcact gggagggcca gctgcttcca cctaagctac 1800
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 aatggtgcat atgcctgag gcttggaaatt gggttgcttt tatgtacaag 1900
 gctagctggg ctttttctc gttgccctga agagacacct gtttgcact 1950

cctctccctg gctgagtcct ctggcatcca tgggtgggtgg tcgagccaag 2000
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 tctcagggtc cctgactgt ggtgcttat cagtgggga gtgtctactc 2500
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<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

	200		205		210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp		
	215		220		225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys		
	230		235		240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met		
	245		250		255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr		
	260		265		270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp		
	275		280		285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu		
	290		295		300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro		
	305		310		315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu		
	320		325		330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala		
	335		340		345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala		
	350		355		360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser		
	365		370		375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala		
	380		385		390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala		
	395		400		405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr		
	410		415		420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala		
	425		430		435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg		
	440		445		450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys		
	455		460		465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys		
	470		475		480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile		
	485		490		495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp Leu	500	505	510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro Phe	515	520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu Ala	530	535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu Phe	545	550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu Ala	560	565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu Val	575	580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu Leu	590	595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro Arg	605	610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu Leu	620	625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu Thr	635	640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser Met	650	655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val Ala	665	670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg Arg	680	685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val Arg	695	700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp Ala	710	715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val Leu	725	730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp Tyr			

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgctgcc gccgctgctg ctgttgcctc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgcc aaacctgcaa acatcacctt 100
cttaccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtcatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaactgggt ccagtggtg gaccaaccac acgctgggtc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgcctagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgttcc tttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgccacaca aggaacatta ttggagtcgc aggcagcgtt 1100
ggcagtcctg ggcccgc aaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggagggggcg 1200
qaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

cctt gatt ccttcgtgt ccagcttcca ccaggattca gagggctgcg 1300
 agc tctga gggggatggg ctgggagagg agggctctct atctaactc 1350
 tggagc cggctccaga cagggccacca ggagaaaatg aaacctatct 1400
 ccttcaatc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450
 gaaacactt ccttttgcct tttgttctct gtgcaaacaa gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttcagt 1550
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 cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atgggtgggc 1650
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 aatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Phe	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
				425					430					435	
Leu	Tyr	Val	Gln	Met	Glu	Asn									
				440											

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
c gctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<200> 1-51
synthetic construct.

<210> 1-51
<211> 150
<212> DNA
<213> Homo sapiens

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
gggaagcgtg ggaggacggc tgggcggacg cgtgggtctc tgcggggaga 50
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tctgctgact gtggccaccg cctgatgctt gcccgtaga gccccgcag 150
gtctctgggg ggccagatc atcgggggccc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttctctgctg cagagccgct ggggtggtctc ggccgcccac tgcctcagcc 300
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gccgtccag gcttgaatg ttcgtggct gggccccac ggaagcctga 1000
tgttcagggt tgggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcnaaggcc aqaagcaaac ccagtaaaat gttactgac aaaaaaaaaa 1100

..... gaaa 1114

<210> 111

<211> 283

..... PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Leu Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 113

cgaagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 114

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<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

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ttttctgtg acggggcgcca acacagqcat cgggaagcag accgccttgg 250
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 tttttaggccc eggcacctgg acttggcttc cctcaagtct atccagaggt 400
 tttttagaaa gatcattgaa gaggaggagc gagtggacat tctaatcaac 450
 aatgggggtg tgatgggtg cccccactgg accacagagg accgcttgcg 500
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<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
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 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	230	235	240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	245	250	255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	260	265	270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	275	280	285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	290	295	300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	305	310	315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	320	325	330

Arg

<210> 117

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 117

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

Ser Pro Glu Asp

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 119
 cgggacagga gacccagaaa ggg 23

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 120
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<210> 121
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 121
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<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

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<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

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				20					25					30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
				170					175					180

Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195

Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210

Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225

Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

230	235	240
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245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
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<210> 125
 <211> 25
 <212> DNA
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<220>
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 <223> Synthetic construct.

<400> 125
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<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
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<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

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<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
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 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Leu	Leu	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gln	Leu	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

129

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<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
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 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	110	115	120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	125	130	135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	140	145	150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	155	160	165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	170	175	180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	185	190	195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	200	205	210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	215	220	225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	230	235	240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	245	250	255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	260	265	270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	275	280	285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	290	295	300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	305	310	315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	320	325	330
Ser	Phe	Leu	Met	Ser											335		

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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 ggcnaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 ggttaacat ttcattcagg aagtcaggta gtgaaactc cttttatcaa 300
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<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
				20					25				30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg
				35					40				45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile
				50					55				60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr
				65					70				75	

Asn	Pro	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asn	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

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Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

10	20	30	40	50	60
Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro	Ala		
65	70	75			
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser	Ala Ile		
80	85	90			
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg	Cys Thr		
95	100	105			
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala	Val Ala		
110	115	120			
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe	Ile Pro		
125	130	135			
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr	Ser Pro		
140	145	150			
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala	Leu Tyr		
155	160	165			
Leu Gly Ile Ile Ser	Ser Leu Phe Ser	Leu Ile Ala Gly	Ile Ile		
170	175	180			
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn	Tyr Tyr		
185	190	195			
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser	Pro Arg		
200	205	210			
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser	Tyr Ser		
215	220	225			
Leu Thr Gly Tyr Val					
230					

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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aggctgtggag acaagatcta caaccctctg gaggcagtgt gttacaatga 200
cgccatcgtg tccctgagcg agaccggcca atgtgggtccc cctgcacct 250
tctggccctg ctttgagctc tctgtctctg attcctttgg cctcacaac 300
gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgcacac 350

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atctcccatc tccagtaaat gtgaaacag aagacgtttt cccagagaag 400
 acatagaag aaatcaact ttcactaagg catctcagaa acataaggcta 450
 aggtaatatg tgtaccagta gagaagccctg aggaattttac aaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 agtgcccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtctgtgccct tggccaggac ccagacgtgt ggaactgca ccttcagagt 250

ctgttttgag cagtgtgtgcc cctggacatt catggtgaa ctgataaacc 300
 agaactggga ctacgcccgg acctcggatg acaggttttg tgcagtgac 350
 acctaatgga acatcagggg aacgatgact cctggattct ccttctctggg 400
 tgggctctga gaaagaggtt ggtgttaact gagatctggg atgttgagtg 450
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 ccttctagaa ttctggacag catgagatgc gtgtgtctgat gggggcccag 600
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105
Cys	Arg	Ser	Val	Ser										
			110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 125 tggca ccagaagttc ctctgcgcgt ccgagggcga catggcgctc 150
 126 tgggcgc tggagggcgg cagctgggcg tggggaacc tgcctctgc 200
 127 tcttctctg gctgcgtccc taggtccggt ggcagccttc aaggctgcga 250
 128 ttccttattc cctgtatgtc tgtcccgagg ggcagaaagt caccctcacc 300
 129 ttcaggtctc tgggcccgtt ggacaaaggg cagcatgtga cctctacaa 350
 130 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
 131 ggcacatccg caacctcag ttcaggacc ttcacctga catggagge 450
 132 caccaggtg ccaacaccag ccacgacctg gctcagcgc accggctgga 500
 133 gtgcgcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 134 cctgtctga tagcggcctc tactgtctgc tggtggtgga gatcaggcac 600
 135 caccactcgg agcacagggt ccattggtgc atggagctgc aggtgcagac 650
 136 aggcaaagat gcaccatcca actgtgtggt gtaccatcc tctcccagg 700
 137 atagtgaata catcagcgt gcagccctgg ctacgggtgc ctgcctcgt 750
 138 ggaatcctc gctccccct catcctgtct ctggtctaca agcaaaggca 800
 139 ggcagcctcc aacgcgcgtg ccagggagct ggtgcggatg gacagcaaca 850
 140 ttcagggat tgaatacccc ggccttgaag cctcaccacc tgcacaggg 900
 141 ataccgagg ccaaagtcag gcaacccctg tctatgtgg ccagcgcca 950
 142 gcctctgag tctgggcggc atctgcttcc ggagcccagc accccctgt 1000
 143 ctctccagg ccccggaac gtctcttcc catcctgga cctgtcct 1050
 144 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100
 145 ttgtggtgg gtctggggca ggtgcatttg agccagggtt ggtctgtga 1150
 146 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200
 147 gatactgtga catcccagaa gccagcccc tcaacccctc tggatgctac 1250
 148 atggggatgc tggacggctc agccctgtt ccaaggattt tggggtgctg 1300
 149 agattctccc ctagagacct gaaattcacc agctacagat gccaatgac 1350
 150 ttacatctta agaagtctca gaagctcag cccttcagca gctctcgttc 1400
 151 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

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 gttgccccac ccactggaga tgggtctgag ggaggtgggt ggggccttct 1850
 gggaaggatg gtggagaggg gcacctgcc cccgcctccc ccactcccta 1900
 ctccactgc tcagcgggg ccattgcaag ggtgccacac aatgtcttct 1950
 ccacctggg acacttctga gtatgaagcg ggaigctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
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 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141

<211> 1732

<212> DNA

<213> Homo sapiens

<400> 141

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ccttctccga ccccgctcta gcagcagacc tcttggggtc tgtgggttga 200
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gagggtctct tcttcttgc tgggaactgc gctgtcttgg ttccccctgg 350
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agatactccc ccggcgagag ctggcaccac tacttggagc cacaaggcct 450

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aaccgctcca ctgtccgctt gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacaaggag 650
agatcttcag tgcccatgag ctgttccctt cccgctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactggggcc tcacaacctg 750
ccccgaacca ggtgcccag cccccctccc actgccagac tctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atgggggtgag acatccctcag gaccatgtt ccagtgtatg 900
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
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ggccagtcca gacaaagtga ccaagacata acaaaagacct aacagttgca 1650
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cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	305	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	320	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser	335	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	350	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	365	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	380	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala	395	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro	410	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala	425	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys	440	450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gctctcggtt atcgtgaccu cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttg cggcgaaggc 350
 ggcgcagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgcgc 400
 gaccttggct tgggcgcagg aatccgagge agcctttctc cttegtgggc 450

cctccggaga gtcgggaccg agataccatg ccaggactct ccgggggtcct 500
 gtcagctgcc gtcgggtgag cactgtttccc ccaaaccttg gaactgaatgc 550
 ttcctggccc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aatgaaaga accaataaaa tcctgttctt ccaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400

154

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ana 1883

<210> 146
 <211> 406
 <212> FRT
 <213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp	1	5	10	15
Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met	20	25	30	
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln	35	40	45	
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn	50	55	60	
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala	65	70	75	
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu	80	85	90	
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro	95	100	105	
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys	110	115	120	
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys	125	130	135	
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg	140	145	150	
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln	155	160	165	
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala	170	175	180	
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala	185	190	195	
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr	200	205	210	
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro	215	220	225	
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln	230	235	240	
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser	245	250	255	

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctctctt tetctctaat ccattccgtca cctctctctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccattggctct catgctcagt 200
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<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

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Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys			
	245		250		255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp			
	260		265		270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys			
	275		280		285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys			
	290		295		300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro			
	305		310		315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val			
	320		325		330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val			
	335		340		345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp			
	350		355		360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His			
	365		370		375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr			
	380		385		390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr			
	395		400		405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe			
	410		415		420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg			
	425		430		435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn			
	440		445		450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu			
	455		460		465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu			
	470		475		480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu			
	485		490		495
Pro Arg Gly Glu	Met				
	500				

<210> 149

<211> 24

<210> DNA
<211> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gggtgggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc aagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgcctt gttgtgctgc gccgcgcgcg ccgcgcgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgggtggcggc ggggcgcgcg ggcaggtgga 250
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caccctcttt tgggcgaatg ctggaccctc ttccaccacc ttccaggcgc 450
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

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				20					25					30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	
				35					40					45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	
				50					55					60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	
				65					70					75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	
				80					85					90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	
				95					100					105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	
				110					115					120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	
				125					130					135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	
				140					145					150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	
				155					160					165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro	

	170		175		180
Arg Thr Glu Ala Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn				
185	190	195			
Cys Ser Val Val Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr				
200	205	210			
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr	Gln Gly Leu His Cys				
215	220	225			
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu					
230	235	240			
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro					
245	250	255			

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 gcttctgttc acagtagcag gccagctgc agaaggacct cactgtgct 550
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 gggcccgaca ccagctcaga ataaagcgtt tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
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 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95				100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile
				110					115				120
Pro	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val
				125					130				135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly
				140					145				150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln	
				155					160				

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cggtgacagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccacccc tcgcattggt ggatttaccc 200
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<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
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Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
	125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu	Ile	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
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 gctcccacc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

	20		25		30									
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
				170										

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggaacctg gtacgtgaag gccatggtagg tcgataagga ctttcaggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatata acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gtccgcaga tgcagaggtt gaggtggctg cgggactgga agtcateggg 50
 cajaggtctc acagcagcca aggaacctgg ggcccgcctc tccccctcc 100
 aggcacagag gattctgcag ttaatcctgc ttgcctctggc aacagggctt 150
 ctagggggag agaccaggat catcaagggg ttgcagtcca agcctcactc 200
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
 cgacgtccat cggccccaga ttgctcctga cagcagccca ctgcctcaag 300
 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
 ctgtgagcag acccggacag ccactgagtc ctccccccac cccggcttca 400
 acaacagcct ccccaacaaa gaccacgcga atgacatcat gctgggtgaag 450
 atggcatcgc cagtcctcat cacctgggct gtgcgacccc tcacctctc 500
 ctacagctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgcctgcctc acaccttggg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
 cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccagggtga ctccgggggc cctctgggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggccagga tccgtgtgag atcacccgaa agcctgggtg 800
 ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggacccacc caccacagcc catcacctc catttccact 900
 tgggtgtttg ttccgtttca ctctgllaat aagaaacctt aagccaagac 950
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
 tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu

1

5

10

15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro		20	25	30
Phe	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu		35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala		50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His		65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr		80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys		95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val		110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys		125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr		140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn		155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly		170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly		185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn		200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala		215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val		230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn							245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
gggtggggga ctggaagta tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcaq 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<21> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cttggatga tectgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatccctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggcttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttctttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcctcgtcc 150

agaaaaactgc totaagacaa gcaagaaggg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atgggttggt cttgggtgtg ggaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca ttgcatatg gaaaggaagg ctatgcagaa 400

ggcagatttc caccggatgc tacattgatt ttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaaaca atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta ctgcaaaagg 550
 gaatttqaaa aagatgagaa gccacgtgac aagtcataac aggatgcagt 600
 tttagaaqat atttttaaga agaattgacca tgatgggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcataatitgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
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 ttgcaaacctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe
1				5					10					15
Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu
				20					25					30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn
				35					40					45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr
				50					55					60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg
				65					70					75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly
				80					85					90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro
				95					100					105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly
				110					115					120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu
				125					130					135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser
				140					145					150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Pro Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgtttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

ccatttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<210>
Artificial Sequence
<211> 1-18
<212> Synthetic construct.

<400> 184
gattgtetgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcattctgat atgaattgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg etttctccag gctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcgc 100

ccaatctgt tctgtgtctc ataacactca ctgcacctgc aacctatgat 150
 atacttttgg atctgggcag aaactattca cattccccctt ggagacatgt 200
 ctgcacagc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aaqccaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggttcacgcc tgcaatccca gttactcggg aggctgagcc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tcctaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgcctctca gtgtttcctg ggatccccctc 550
 ccaataaaq tacttatatt etc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 192
 cctgtgctaa gtgcaccca aatgcttcc tgttcaataa cactcactgc 50

<210> 193
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 193
 caagcaggtc atcccttgg tgaccttcaa agagaagcag agagggcaga 50
 ggtggggggc acagggaaaag ggtgacctct gagattcccc ttttccccc 100
 gactttggaa gtgacccacc atgggggtca gcatcttttt gctcctgtgt 150
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
 gtgtgggggt aactcacagc cgtggcaggt ggggtgttt gagggcacca 250
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
 gctcactgca ggggcagcag gtactgggtg cgcctggggg aacacagcct 350
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
 cccatcccggt ctacctggga gcctcgacga gccacgagca cgacctccgg 450
 ctgctgcggc tgcgcctgac cgtccgcgta accagcagcg ttcaacctct 500
 gcccttgccc aatgactgtg caaccgctgg caccgagtgc cactctcag 550
 gctggggcat caccaaccac ccacggaacc catcccgga tctgtccag 600
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
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 atgcctgcca qggtaattct gggggccccc tgggtgtgtg gggagtcctt 750
 caaggtctgg tctctgggg gtctgtggg cctgtggac aagatggcat 800

cctggagtc taaactata ttgcaagta tgggactgg atccqatga 850
 tctgggga aaactgaact gtttctcca cctcaccac cacccttaa 900
 attgggacc cctctgccc tcagagcacc aatactctct ccataccttc 950
 acctagctcc actcttggtt gccctgggaac ttcttggaac tttaactct 1000
 gcaacccctt ctaagaccca cgagcggggt gagagaagtg tgcataagtc 1050
 tggataaat ataatgaag gaggggcaaa aaaaaaaaa a 1091

<10> 194
 <11> 248
 <212> PRT
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccggg ccadggccct gtgcctcctc 50
 ctctctcctc gcccgctccg cgaagccttg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
 ggcttgctca aagccccgca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaaqt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgaacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccacac ctggagatga aqaagatgat ctacagagtg acaggagggg 400
 tcagtgcacac tatatccac ccagactttg tgaacatgat gctggggaaa 450
 ccgtcggtctg tctcaagtt agtcatgatg ttggaaggaa aagccaacga 500
 gacagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgcctccctt ctlgacacac tglgatctct ctctctctca 650
 tttgtttggt cattgagggt ttgtttgtgt ttcatcaat gtctttgtaa 700
 agcacaatt atctgcctta aaggggctct gggtcgggga atctgagcc 750
 ttgggtccc tccctctctt ctccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850
 ctccagcct gtgttccct cacttgagg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gticaggctc actgacctgg ctctgacgag 950
 gaccccaggc cactctgaga agaccttga gtagggacaa ggcctgcaggg 1000
 cctctttcgg gtttctttgg acagtgcat gggtccagtg ctctggtgtc 1050

atccacagaca cagccactcg ggcccceqat gcccacagctg atccccaactc 1100
 attccacacg tctttctcatc ctcaqfcatg tgaaggttgg aagdaaaagga 1150
 ttttgcattt gggagccctt caagaaggtt caagaaggaa cctccacagtc 1200
 atgctctctg gccacacctg tgcagggcagc tgagagggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgcagccc 1300
 tgggggtttg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe					
1				5					10					15					
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn					
				20					25					30					
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu					
				35					40					45					
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp					
				50					55					60					
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met					
				65					70					75					
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys					
				80					85					90					
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr					
				95					100					105					
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu					
				110					115					120					
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro					
				125					130					135					
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro					
				140					145					150					

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

400-197

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cggggcctcc cccgaacgc tgcgcctct gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaaaaa ctcggagct 350
tgcctctgga agacaaccag gtcagcctca tgcagagagg cgccttccag 400
gacctgaacg agctagagcg actgcgcctg aacaagaata agctgcaagt 450
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<210> 198
 <211> 1523
 <212> PRT
 <213> Homo sapiens

<400> 198
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 20 25 30
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
 35 40 45
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
 50 55 60
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
 65 70 75
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
 80 85 90
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
 95 100 105
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
 110 115 120
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
 125 130 135
 Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
 140 145 150
 Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
 155 160 165

Asn Asn His Ile	Ser Cys Ile Glu Asp	Gly Ala Phe Arg Ala	Leu
170		175	180
Arg Asp Leu Glu	Ile Leu Thr Leu Asn	Asn Asn Asn Ile Ser	Arg
185		190	195
Ile Leu Val Thr	Ser Phe Asn His Met	Pro Lys Ile Arg Thr	Leu
200		205	210
Arg Leu His Ser	Asn His Leu Tyr Cys	Asp Cys His Leu Ala	Trp
215		220	225
Leu Ser Asp Trp	Leu Arg Gln Arg Arg	Thr Val Gly Gln Phe	Thr
230		235	240
Leu Cys Met Ala	Pro Val His Leu Arg	Gly Phe Asn Val Ala	Asp
245		250	255
Val Gln Lys Lys	Glu Tyr Val Cys Pro	Ala Pro His Ser Glu	Pro
260		265	270
Pro Ser Cys Asn	Ala Asn Ser Ile Ser	Cys Pro Ser Pro Cys	Thr
275		280	285
Cys Ser Asn Asn	Ile Val Asp Cys Arg	Gly Lys Gly Leu Met	Glu
290		295	300
Ile Pro Ala Asn	Leu Pro Glu Gly Ile	Val Glu Ile Arg Leu	Glu
305		310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala	Gly Ala Phe Thr Gln	Tyr
320		325	330
Lys Lys Leu Lys	Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335		340	345
Ile Ala Pro Asp	Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser	Leu
350		355	360
Val Leu Tyr Gly	Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu	Phe
365		370	375
Asp Gly Leu Val	Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn	Lys
380		385	390
Ile Asn Cys Leu	Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn	Leu
395		400	405
Asn Leu Leu Ser	Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser	Lys
410		415	420
Gly Leu Phe Ala	Pro Leu Gln Ser Ile	Gln Thr Leu His Leu	Ala
425		430	435
Gln Asn Pro Phe	Val Cys Asp Cys His	Leu Lys Trp Leu Ala	Asp
440		445	450
Tyr Leu Gln Asp	Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys	Ser

455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser		
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe		
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg		
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg		
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn		
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys		
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys		
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu		
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val		
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn		
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser		
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr		
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu		
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly		
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys		
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala		
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760						765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775						780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790						795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805						810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820						825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835						840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850						855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865						870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880						885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895						900
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910						915
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925						930
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940						945
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
				950					955						960
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970						975
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985						990
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000						1005
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015						1020
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
				1025					1030						1035
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

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Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Gln Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
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 Glu Cys Gly Cys Leu Ala Cys Ser
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<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<21> Artificial Sequence
<22> 1-24
<23> Synthetic construct.

<400> 200
tttttggaat tgaggaggag cagg 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcacag tcgaaataag cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
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gtttcttccg cagactcaac tgagaagtea gctcttgggg caggcaccag 100
gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gacctcatt ggtgcctgg tcacaggcgc cgaatccaaa 200
atctacactc gttgcaaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggtca caacaccaca gcccgcagg tctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgccg ggaatttgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtccgt ttctcccaa tattcctctt caaacttga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
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 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
 ctcttggtt gactgtatc aggc 24

<210> 206
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 206
 ccagtcggac aggtctctcc cctc 24

<210> 207
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 207
 tcagtgaacca aggtcagca ggcg 24

<210> 208
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 208
 ctacactcgt tgcaaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
 <211> 1648
 <212> DNA
 <213> Homo sapiens

<400> 209
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 tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
 gcggaagaag atccatthttt actgtcaactt cccagatctg cttctcacca 250

$$\begin{aligned} \langle 210 \rangle & 210 \\ \langle 211 \rangle & 323 \end{aligned}$$

ERT
me sapiens

110
Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
5 10 15
Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30
Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45
Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60
Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75
Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90
Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105
Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120
Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135
Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150
Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
155 160 165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
170 175 180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
185 190 195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
200 205 210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
215 220 225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
230 235 240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
245 250 255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
260 265 270

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
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 tctaccteta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggag 200
 tttgcattgag ttcttggta atttgcattg gagatatggg cctgtgggtct 250
 ccttctggtt tggcagggcg ctctgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atataatcc caataagaca tgggacctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tggtaggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccttctctct aaagcttcca gaagaattat tagataaatg 500
 gctctctac ccagagaccc agcagtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg ctccagaag aatcatggca cagtttggtc 650
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 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
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 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaaagagata aaccaagttt ttggaaatgg tctgttact ccagagaaaa 1000

tttataggt cagatattgt cagcatgtgc ttgtgaaac tgttcgaact 1050
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 tgaacagattt attattctta gagagacccct cgtccctttat gcccttggtg 1150
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 gatgggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctccaggaca caggagtgc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggate actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgtttaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatccittta taaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1				5					10					15

Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30

Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45

Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60

Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75

Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90

Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105

Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120

His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135

Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Gln Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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 tcaaggcttg tgcctctcgg ctctctgaag ctcttggcgc atctgggtgt 150
 cgtcatcacc ttattcttgt cccgggacag caacatacag gcttgcctgc 200
 ctctcacgtt ccccccgag gactatgaca agcaggacat tcagetgggtg 250
 gcccgcctct ctgtcacctt ggccctcttt gcagtgagac tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagccctc atctccattg 350
 gggtcactg tagtgcctcc gtggccctgt ccttcttcat attcagagct 400
 tggagtgca ctacgtattg gtacattttt gtctctctga gtgccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacctctctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600
 ttccctcggg aaactgcttc tgcctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtctttg taataaaata 700
 tgtttttag taacattaag acttatatac agtttttaggg gacaattaaa 750
 aaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met	Gly	Arg	Val	Ser	Gly	Leu	Val	Pro	Ser	Arg	Phe	Leu	Thr	Leu
1				5				10						15
Leu	Ala	His	Leu	Val	Val	Val	Ile	Thr	Leu	Phe	Trp	Ser	Arg	Asp
			20					25						30
Ser	Asn	Ile	Gln	Ala	Cys	Leu	Pro	Leu	Thr	Phe	Thr	Pro	Glu	Glu
			35					40						45

17. Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr			
			50					55					60			
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val		
			65					70					75			
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His		
			80					85					90			
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp		
			95					100					105			
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu		
			110					115					120			
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu		
			125					130					135			
Lys	Lys	Lys	Pro	Phe												
			140													

<210> 215

<211> 697

<212> DNA

<213> Homo sapiens

<400> 215

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ggcatcagag tgcggccagc acctgagcct gcccttacgc tatgtggtgg 200
tatccacac ggcgggcagc agctgcaaca ccccgacctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtgca 300
cgtgggctac aacttcttga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcacacacc 450
ccaggccatc cgggcagccc agggctctact ggctgcggt gtggctcagg 500
gaaccttgaq gtccaactat gtgctcaaag gacacgggga tgtcagcgt 550
acactctctc caggcaacca gctctaccac ctatccaga attggccaca 600
ctaccgctcc cctgaggccc ctgctgctcc gcacccatt cctccctcc 650
catggccaaa aaccccatg tctctctctc caataaagat gtaqctc 697

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<210> 216

<211> 196

<212> FRT

[illegible]

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<210> 217
<211> 1871
<212> DNA
<213> Homo sapiens
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tctatctggt catctgtggc caggatgatg gtctctccgg ctacagaggac 150
cctgagcgtg atgaccaaga gggccagccc cggccccggg tgcctcggaa 200
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gggggggccc atctcaacta agtcggccc catggcatt tccctctctc 250
 tagggctgct gggggggccc ggggaggtt ggggcattct tgggcagccc 300
 ccccaacggc cgaaccacag ccccccaccc tcagccaaag taaagaaaat 350
 ctctggctgg ggcgaattct actccaacat caagaagggt gccctgaacc 400
 tgcctgtcac aggggaagatt gtggaccatg gcaatgggac ctccagcgtc 450
 nacttccaac acaatgccac agggcagggg aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcctcg 550
 aagccaaagg ctccaaaatc ttcaactgcc ggatggagtg ggaagaaggta 600
 gaacggggcc gccggacctc gctttgcacc caagacccag ccaagatctg 650
 ctcccagac caagctcaga gctcagccc ctggagctgc tcccagccct 700
 tcaaagtcgt ctgtgtctac atgccttct acagcacgga ctatcggtg 750
 gtccagaagg tgtgcccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccggggg caggccacag agggcagggc aqggtctqaa 850
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 aaccgtgat tctgacttt tgtgtgaaga atcgtgttct tggaccagga 1850
 aataaagctt gcccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218
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 Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
 20 25 30
 Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45
 Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50 55 60
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80 85 90
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
 110 115 120
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
 125 130 135
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
 140 145 150
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
 155 160 165
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
 170 175 180
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
 185 190 195
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
 200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219
<211> 2065
<212> DNA
<213> Homo sapiens

<400> 219
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gggtttctgca tgagctcctt aaaggacaaa ggtaacagag ccagecagag 150
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 ttcaaatatc ccatatctaa atttagtgca atatcttgct ttttgtatag 2000
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 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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 20 25 30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
 35 40 45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
 50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	65	70	75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	80	85	90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	95	100	105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	110	115	120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	125	130	135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	140	145	150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	155	160	165
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	170	175	180
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	185	190	195
Phe	Leu	Val	Phe	Pro	Leu										200		

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
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<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
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<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
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<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	1	5	10	15
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	20	25	30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	50	55	60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	95	100	105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	110	115	120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	125	130	135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	140	145	150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	155	160	165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	170	175	180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	185	190	195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	200	205	210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	215	220	225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	230	235	240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	245	250	255	
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<216> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Asp	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Phe	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

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Leu Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335		340		345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350		355		360
Pro Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365		370		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380		385		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395		400		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys	410		415		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala	425		430		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe	440		445		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val	455		460		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn	470		475		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly	485		490		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile	500		505		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile	515		520		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu	530		535		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr	545		550		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys	560		565		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met	575		580		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro	590		595		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile	605		610		615

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Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
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Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
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Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
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Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
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Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
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His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
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Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
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<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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 gtagaagccc ctccatctgc cctgggggtg aggcaccatc accatcacca 2700
 ggcattgtct cagagccttg acaccaactt tatggactgc ccatgggagt 2750
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 ctggggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaq 2848

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1					5				10					15

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20										25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Asp	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Pro	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile		
			335					340					345		
Ile	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
			350					355						360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
			365					370						375	
Glu	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
			380					385						390	
Ile	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
			395					400						405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
			410					415						420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
			425					430						435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
			440					445						450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
			455					460						465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
			470					475						480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
			485					490						495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
			500					505						510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
			515					520						525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
			530					535						540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
			545					550						555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
			560					565						570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
			575					580						585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
			590					595						600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

	605	610	615
Glu Val His Thr	Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
	620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
	635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		
	650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
	665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
	680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
	695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
	710	715	720
Pro Val Val Val	Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
	725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
	740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
	755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
	770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
	785	790	795
Gln Pro Ala Asp	Ser Val Pro Leu Lys Ala Thr Val		
	800	805	

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgccttaccg cgcagcccca agattcacta tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aaccccaactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
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 atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
 acttgaagct caattttctg aaatctccct cctccttcaa tgggctctg 200
 gatgtcctgg tcccatctgt cagtctgcag gcatttaaat ccttcttgag 250
 atcccagggc ttagagtaac cagtgcacat tgaggacctg caggcccttt 300
 tagacaatga aatgatgaa atgcaacaca atgaagggca agaacggagc 350
 agtaataaet tcaactacgg ggettaccat tccctggaag ctatttaacca 400
 cgagatggac aacattgccg cagactttcc tgaacctggcg aggaggggtga 450
 agattggaca ttggtttgaa aaccggccga tgtatgtact gaaattcagc 500
 actgggaaaag gctgaggcg gccggccgtt tggetqaatg caggcatcca 550
 ttcccgaag tggatctccc aggccactgc aatctugacg gcaaggaaga 600
 ttgtatctga ttaccagagg gatccagcta tcacctccat ctggagaaa 650
 atggatattt tcttgttgc tgtggccaat cctgatggat atgtgtatac 700
 tcaaaactca aaccgattat ggaggaagac ggggtccga aatcctggaa 750
 gctcctgcac tgggtctgac ccaaatagaa actggaacgc tagttttgca 800
 ggaaaggag ccagcgacaa cctttgctcc gaaqtgtacc atggaccca 850

cgcacattcg gaagtggagg tgaattcaat ggtagatttc atccaaaaac 900
 atgggaattt caagggcttc atcgacctgc aaagctactc gcaagctcctg 950
 ctgtatccat atgggtactc agtcaaaaag ggcacagatg ccgagggaact 1000
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 agcagcctcg actgggcgta tgacaacggc atcaaatltg cattcacatt 1150
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 ttactctct ctctcctltg ttattcagtg tgaccaggat ggcgggaggg 2250
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 agctgcctct tgtttcattt caccacagca cgtaccatct gtcttttgt 2650
 tgttgttqtl ttgttttltg ttttttgcct ttaccaaaaca tgtctgtaaa 2700
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile
			170					175					180
Arg	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala
			185					190					195
Ile	Leu	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr
			200						205				210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn
			215						220				225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg
			230						235				240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp
			245						250				255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser
			260						265				270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser
			275						280				285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly
			290						295				300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu
			305						310				315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu
			320						325				330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser
			335						340				345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val
			350						355				360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly
			365						370				375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr
			380						385				390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu
			395						400				405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn
			410						415				420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

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tgttccaaaa tggcatctta cctttatgga gtactcttgg ctgttggcct 100
ctgtgtctca atctactgg tgtccccggc caatgcccc agtgcatacc 150
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtartccctc 200
aacaccgaact ttgccttccg cclataccgc aggetggttt tggagacccc 250
gagtcagaac atctctctct cccctgtgag tgtctccact tccctggcca 300
tgtctccctt tggggccccc tcagtcacca agacccagat tctccagggc 350
ctgggcttca aactcacaca cacaccagag tctgccatcc accagggctt 400
ccagcacctg gttcaactca tgaactgtcc cagcaaaagc ctgacctga 450
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tgacaaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400
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 ...agca acccaggtta ggcacctcta ttgcagaat; acaataaac 1650
 atttaataaa actaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aatataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<111> 236
 <111> 417
 <212> PRT
 <113> Homo sapiens

<400> 236
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
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 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

	200		205		210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe		
	215	220	225		
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met		
	230	235	240		
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn			
	245	250	255		
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe		
	260	265	270		
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala		
	275	280	285		
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys		
	290	295	300		
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser		
	305	310	315		
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala		
	320	325	330		
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser		
	335	340	345		
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser		
	350	355	360		
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile		
	365	370	375		
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn		
	380	385	390		
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile		
	395	400	405		
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser			
	410	415			

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctggtt ggctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg qaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttgccctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgacggt gctacattgc ctggagggaag cctaagggaac ccaggcatcc 50

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 ggacccaggc atcttgcttt ccagccacaa agagacagat gaaqatgcag 250
 aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300
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 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

	365		370		375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380		385		390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395		400		405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410		415		420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425		430		435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440		445		450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455		460		465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470		475		480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485		490		495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500		505		510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515		520		525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530		535		540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545		550		555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560		565		570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575		580		585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590		595		

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

<400> 245
atctgacag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gttaggttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggaccacaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaaatagca gcgtagcttc cctggctcct ctctgcatcc 50

tccccgacct tcccagcaat atgcatcttg caagtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatggggcg ccagcgatga 150

ccccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttag acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450

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ctgggaagga agcagagaaa ctgggccaag gggtaacca tgctgctgac 550

caggctggaa aggaagtggg gaagcttggc caaggtgccc accatgctgc 600

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 tttttttt cctgaaggg ggttgtactg ggatttgtga ataaacttga 950
 taccaca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu
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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu
				20					25					30
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg
				35					40					45
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His
				50					55					60
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met
				65					70					75
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu
				80					85					90
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile
				95					100					105
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn
				110					115					120
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln
				125					130					135
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys
				140					145					150
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu
				155					160					165
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala
				170					175					180

Asp	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
			185					190					195
Thr	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
			200					205					210
His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly	
			215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp
			230						235				240
Ser	Val	Ala	Asn	Ile	Met	Pro							
			245										

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caataatgcatt cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgaccccaatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

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 100 tccaggaaga ggggccccgc ggggggggat gaccgtgcgc
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 gtttgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

	80		85		90
	Gln Leu Ser Ser Asn Leu Ser Phe	Leu Pro Gly Gly Glu Tyr			
	95	100			105
Gln Leu Leu Trp Gly Ala Asp Ala	Glu Lys Lys Gln Gln Cys				
110	115				120
Leu Phe Lys Gly Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr Ile				
125	130				135
Lys Ile Leu Leu Pro Leu Ser Gly Ser	His Leu Phe Thr Cys Gly				
140	145				150
Thr Ala Ala Phe Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu Asn				
155	160				165
Phe Thr Leu Ala Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu Asp				
170	175				180
Gly Lys Gly Arg Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr Ala				
185	190				195
Leu Val Val Asp Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser Phe				
200	205				210
Gln Gly Asn Asp Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg Pro				
215	220				225
Thr Lys Thr Glu Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala Phe				
230	235				240
Val Ala Ser Ala Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln Gly				
245	250				255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe	Ser Glu Thr Gly Gln Glu				
260	265				270
Phe Glu Phe Phe Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg Ile				
275	280				285
Cys Lys Gly Asp Glu Gly Gly Glu Arg	Val Leu Gln Gln Arg Trp				
290	295				300
Thr Ser Phe Leu Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp Asp				
305	310				315
Gly Phe Pro Phe Asn Val Leu Gln Asp	Val Phe Thr Leu Ser Pro				
320	325				330
Ser Pro Gln Asp Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe Thr				
335	340				345
Ser Gln Trp His Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys Val				
350	355				360
Phe Thr Met Lys Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr Lys				
365	370				375

Gln	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Ile	
				380					385					390	
Val	Ile	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	
				395					400					405	
Gln	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Ile	Asp	Arg	Val	Leu	
				410					415					420	
Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser	
				425					430					435	
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala	
				440					445					450	
Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	Phe	
				455					460					465	
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	
				470					475					480	
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	
				485					490					495	
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	
				500					505					510	
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	
				515					520					525	
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	
				530					535					540	
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	
				545					550					555	
Tyr	Gln	Pro	Gln	Leu	Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	
				560					565					570	
Gly	Ala	Ser	Ala	Lys	Asp	Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	
				575					580					585	
Pro	Ser	Phe	Val	Pro	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	
				590					595					600	
Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser	
				605					610					615	
Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	Asn	Gly	Ala	Pro	Val	Asn	
				620					625					630	
Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	Gly	Asp	Leu	Leu	Leu	
				635					640					645	
Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu	
				650					655					660	
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val	

	665		670		675
Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro		
	680		685		690
Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys		
	695		700		705
Asp Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val		
	710		715		720
Met Lys Thr	Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe		
	725		730		735
Leu Leu Tyr	Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln		
	740		745		750
Gly Glu Cys	Ala Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu		
	755		760		765
Pro Pro Glu	Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr		
	770		775		780
Pro Leu Asp	His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro		
	785		790		795
Gly Ala Arg	Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile		
	800		805		810
Gln Asp Ser	Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg		
	815		820		825
Val Arg Leu	Gly Ser Glu Ile Arg Asp	Ser Val Val			
	830		835		

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccggtgca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<210> 255
 ctggcagg gcagcgctcc ctgg 24

 <210> 256
 18
 <212> DNA
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 <220>
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 <222> 1-18
 <223> Synthetic construct.

 <400> 256
 gtgagcgctg cagttggc 18

 <210> 257
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 <222> 1-41
 <223> Synthetic construct.

 <400> 257
 agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

 <210> 258
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-45
 <223> Synthetic construct.

 <400> 258
 gagctgcaga tcttctcacc gggacagccc gtgcagaatc tqctc 45

 <210> 259
 <211> 4563
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 3635
 <223> unknown base

 <400> 259
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 cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100

 agggcgggac gggagcccgg actcgctctgc cgcgcgcgtc gtcgcgcgtc 150

191 ggcccc gggccccgc gggggagggg gggggagggc cggcaacctcg 200
 192 gggagcc gccgctagcg cggggcgggc atggtccctt cttaaaggcg 250
 193 gggggggg cggggggggc ggggtgtggg aacaaaggcg cggggcgggg 300
 194 gggggggg gtcggggggc cgggatggc ggggggggc cggggggggc 350
 195 gggggggc cggggcggg cctcggggg ctaggggggg ctggcctcgg 400
 196 gggggggg caggcgggtg agggcggcg gaggctcgg cggcggggc 450
 197 gggggggg gggggccggc ggggggagcg gggggggcat ggccggcgcg 500
 198 gggggcgcg cctggctcag cgtgctgctc gggctcgctc tgggttctgt 550
 199 gctggcctcg cggctcgctc tggcccggc ttccgagctg aagcgagcgg 600
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 214 tgagatgcgg cagctttttt atgagaatta cgaacagaa aaaaaggggt 1350
 215 acattagaga tctccataac agtaaaattc accaagctat cacattacac 1400
 216 cccaacaaaa acccacccta ccagtacagg ctccacagct acatgctgag 1450
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 218 ttgtctgat gagcaaatc agcaacacag aaattcataa agaggacctc 1550
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aatgatca ggttttgcct ttgaacacat cttcttgcgtg aacattatgt 3100
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 ccagtgaaca atattttct attgtacttt tcgaaccatt ttgtctcatt 4500

atttcctgttt tagctgaaga atttgtattac atttggagag taaaaaactt 4550
 aaacacgaaa aaa 4563

<211> 260
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 260

Met	Ala	Ala	Arg	Gly	Arg	Arg	Ala	Trp	Leu	Ser	Val	Leu	Leu	Gly	1	5	10	15
Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	20	25	30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	35	40	45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	50	55	60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	65	70	75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	80	85	90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	95	100	105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	110	115	120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	125	130	135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	140	145	150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	155	160	165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	170	175	180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	185	190	195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	200	205	210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	215	220	225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	230	235	240	

Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	245	250	255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	260	265	270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	275	280	285
Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala	290	295	300
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu	305	310	315
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg	320	325	330
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser	335	340	345
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro	350	355	360
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu	365	370	375
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly	380	385	390
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu	395	400	405
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala	410	415	420
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly	425	430	435
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp	440	445	450
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val	455	460	465
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile	470	475	480
Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys	485	490	495
Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser	500	505	510
Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu	515	520	525
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu			

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Leu Gly Arg Phe	Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu		
	545		550		555
Lys Thr Cys Leu	Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu		
	560		565		570
Leu Phe Asn Ser	Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu		
	575		580		585
Leu Met Arg Asp	Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln		
	590		595		600
Ile Leu Pro Val	Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu		
	605		610		615
Val Gly Ser Ser	Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys		
	620		625		630
Asp Val Asp Leu	Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg		
	635		640		645
Ala Asn Thr Val	Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile	Phe		
	650		655		660
Ser Gln Tyr Asp	Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser		
	665		670		675
Asp Asn His Phe	Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn		
	680		685		690
Tyr Gly Phe Gly	Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg		
	695		700		705
Val Gly Gly Phe	Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp		
	710		715		720
Val Asp Leu Phe	Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe		
	725		730		735
Arg Ser Gln Glu	Val Gly Val Val His	Val His His Pro Val	Phe		
	740		745		750
Cys Asp Pro Asn	Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly		
	755		760		765
Ser Lys Ala Ser	Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met		
	770		775		780
Trp Leu Glu Lys	Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn	Asn		
	785		790		795
Asn Gly Ser Val	Arg Thr Ala				
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<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tcttcaatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20				25					30	
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35				40					45	
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser

	50		55		60
His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	65		70		75
Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80		85		90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95		100		105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110		115		120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125		130		135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140		145		150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155		160		165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170		175		180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185		190		195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200		205		210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215		220		225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230		235		240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245		250		255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260		265		270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275		280		285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290		295		300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305		310		315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320		325		330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335		340		345

Met Leu Lys Val Tyr
350

210 266

1403

1128 DNA

213 Homo sapiens

1480 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

	20	25	30
Pro Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu	35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe	50	55	60
His Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser	65	70	75
Lys His Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp	80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr	95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile	110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly	125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile	140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg	170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile	185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu	200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu	215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu	230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile	245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys	290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro	305	310	315

Val	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330	
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

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<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 ... 2103

216 169
 211 423
 212 PRT
 Homo sapiens

216 169
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 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
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 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
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 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
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 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
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 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
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 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
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Thr	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Arg	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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			20					25					30	
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40					45	
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
			50					55					60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
			65					70					75	

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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 actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
 taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

ctggtctttt qgaagtatt ataagaaaat ttgcacataa 2000
 ctggtgat tcagaaagga cttgtatgct gttttttccc caaatgaaga 2050
 ctggtaga cactaaacac ttttataaaa gcttatcttt gctttctcca 2100
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 ctggtttat taaatttttt tacaagagta tagtatattt atttgaatg 2300
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<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273
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 20 25 30
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
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<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

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 ttctgacctg ctggccagcc aggaactgtg tggggaggcc ctctgctgc 150
 cttggggtga caatctcagc tccaggctac agggagaccg qgaggatcac 200
 agagccagca tgttacagga tctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
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 aacagcccag gagcttgcg ttgggaactc aagtgggccc tgtctctcag 750
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213 275
211 432
    PRT
213 Homo sapiens
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Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	260	265	270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	275	280	285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	290	295	300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	305	310	315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	320	325	330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	335	340	345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	350	355	360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	365	370	375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	380	385	390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	395	400	405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	410	415	420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu				425	430	

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 <211> 3143
 <212> DNA
 <213> Homo sapiens

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<210> 277
 <211> 761
 <212> PRT
 <213> Homo sapiens
 <400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro			

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
305	310	315
Leu Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Pro	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Pro	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Ile	Ile	Ile	Val	Gln	605	610	615
Arg	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Ile	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala					755	760	

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

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<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

79
at ggtgttccac ccag 24

<210> 280

<211> DNA
<212> Artificial

<213>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
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<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
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ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
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117 sapiens

160-242

Met	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Thr
				20				25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln
				35				40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys
				50				55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr
				65				70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe
				80				85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg
				95				100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu
				110				115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu
				125				130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr
				140				145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala
				155				160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile
				170				175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His
				185				190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser
				200				205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr
				215				220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His
				230				235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala
				245				250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly
													Gly

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Asn Met Glu Lys	Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu	Asn		
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Leu Ile Ala Lys	Phe Gly Asp Ser Gly	Phe Val Leu Val Thr	Leu		
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Asn Ser Met Val	Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys	Glu		
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Met Asn Asn Ala	Phe Ala His Leu Pro	Gln Gly Val Ile Trp	Lys		
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Cys Gln Cys Ser	His Trp Pro Lys Asp	Val His Leu Ala Ala	Asn		
	335		340		345
Val Lys Ile Val	Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala	His		
	350		355		360
Pro Ser Ile Arg	Leu Phe Val Thr His	Gly Gly Gln Asn Ser	Ile		
	365		370		375
Met Glu Ala Ile	Gln His Gly Val Pro	Met Val Gly Ile Pro	Leu		
	380		385		390
Phe Gly Asp Gln	Pro Glu Asn Met Val	Arg Val Glu Ala Lys	Lys		
	395		400		405
Phe Gly Val Ser	Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr	Leu		
	410		415		420
Ala Leu Lys Met	Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys	Ser		
	425		430		435
Ala Ala Val Ala	Ala Ser Val Ile Leu	Arg Ser His Pro Leu	Ser		
	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile	Asp His Val Leu Gln	Thr		
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr	Val Phe Gln Gln Pro	Trp		
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe	Val Phe Leu Leu Gly	Leu		
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met	Ala		
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Val Trp Trp Leu	Arg Gly Ala Arg Lys	Val Lys Glu Thr			
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 <212> DNA
 <213> Artificial

<210> Artificial Sequence
<211> 1-24
<22> Synthetic construct.

<400> 283
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<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcagqctggt ctccaaagag aagg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
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<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

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1	Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser		
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<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
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<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
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<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
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492

281

260	265	270
Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Glu Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial

<220>

1. Artificial Sequence

1-50

2. Synthetic construct.

3. 295

aaqaalgaat tgtacaaagc aggtgatctt cgaagagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Trp	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttctctctgt ggggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<21> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gctacccca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgtcctgggg cagccaccag gcatattcat ctttgttgtt gttttcttt 100
tgcttttagca ctggggcaact tcttgcttat ttcttttgta ggaaaggggc 150
tcagtttgct ttgtggggtt ggtggcaggc aggcggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
tagctggggt ctgagacctg ctccctcagt aaaattcctg ggaletgcct 300
ataccttctt ttctctaacc tggcatacce tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
tctttggctg gacactgttc cctgcccccc ccatactctt cctaactaat 550
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
ctggcctgac agaattctat cttgtttaat gctctcataa gaccacttgt 650
ttcccttttg cagcaattgc cactcagttg tatctttatg tgcgtttgtg 700
gttgatatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

agntcaagg gcattgctgt gctgcccagg tatagtgcct acatgtgatg 800
 agtgcfcattg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 caatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 ccttactgtt gcttgtgaat tatctgggga tgcaggctct gattcagtag 950
 tccagggttg ggcattctca aaaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagcccagg ctgggcatgg 1050
 aggtcacac ctatgatccc agcaccttgg gaggtcaggg caggetgate 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaaaccca 1150
 tctgtactaa aaatacaca attagctggg catggtggca catgctgta 1200
 gtcccagcta ctggggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggaqgttg cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20						25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
			35						40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
			50						55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
			65						70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
			80						85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
			95						100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
			110						115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
			125						130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

203
 2211-1768
 DNA
 1.3- Homo sapiens

4.0- 303

at tgaactg gaactcctgg tcccaagtga tccaccgccc tcagcctccc 50
 aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 ttcttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatctctgtg tggetagtgc tctactcct acctacatta aaatctgttt 200
 ttctctctct tctaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaac tgaccttcac tctggaacga gaacagaggt 300
 ttctacccac accgtccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcctgtg agcagtgcct tcaccaactg tctcagctct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggttg acaagcccga agatttcata 500
 ggcgatggct cccactgcct aggcctcagc cttgctgtag tcaatcactg 550
 ccttggggcc aggaaggccc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gccgcgccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccact ggtttatgtg 750
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 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
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 ggaagggtg ccgatgggc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccag taccagctgc tgaagggcaa 1000
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tcttccagct aagcacaggc tgcacaaatcc ccaggcaaaag gactgtgtgg 1300
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 ggagaattact tgaacctggg aggtgaagga ggttgagaca ggagaatcac 1700
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 aattatgggt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

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 tcttctgac tccgcgcgc tctgcgcgc gccatgacc agccggtgcc 100
 tctctcc gtgcgcgcgc cgttgcgcct gggtccagcc gcaactggcg 150
 cctcttgcg caactggcct tctctgggga ggcggtgcc cccatggcga 200
 tcttgggag agcagtgcct gcttccccc gaggacagcc gctgtggca 250
 gtctctctg agccgtcca tgcgggagca cccggcctg cgaagcctga 300
 gcttctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
 cagggccagc tcttggccaa cctggcgcg ctcctccagg ccaagaaggc 400
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 cgaactccgg ctgaagccc ccttggagac cctggacgag ctgctggcgg 600
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 aactgtccg cctactacga gcctgcctg cagctgctgc gaccgcgagg 700
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 cgaaaagggga cgtggcgccc gactgtgtgc gaaacctaaa cgaacgcac 800
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850
 cactttggcc ttcaagatct agggctggcc cctagtgaat gggctcgagg 900
 gaggggtgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala
 1 5 10 15

Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
 20 25 30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
 35 40 45

Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
 50 55 60

Arg Leu Leu
75

Cys Glu Gln
90

Ala Lys Lys
105

Leu Ala Leu
120

Cys Glu Val
135

Arg Gln Ala
150

Ala Leu Glu
165

Thr Phe Asp
180

Ala Tyr Tyr
195

Leu Ala Val
210

Pro Lys Gly
225

Arg Ile Arg
240

Gly Asp Gly
255

ctgggc 50

ctgttc 100

catcgc 150

cttttg 200

cacgac 250

cttaag acaagtacgg gaaqcccaac aagaggaaag gcttcaatga 300
 ctgtgtgg gagatccaga acaaccccca cgcagctac agcgccttc 350
 ctctctag ctctccgac agcgaggccc ccgaggccaa ccccqccgac 400
 ctctctag ctgaagagga cgaatgaggac cggggggtca tggccgtcac 450
 ctgtaac gccacagctg ccagcgacag gatggagagc gactcagact 500
 taqccagag taqcgacaac agtggcctga agaggaagac gcttgcctca 550
 aagatgtcgg tctcgaaacg agcccgaaag gctccagcg acctggatca 600
 aaccagcgtg tccccatccg aagaggagaa ctcggaagc tcctctgagt 650
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 aggtggagcg gacccggaag cggtcgagg gcttctcgat ggacaggaag 1450
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 gcaagacaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200
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 actataaacg gttttttaat ga 2272

<210> 308
 <211> 671
 <212> PRT
 <213> Homo sapiens

<400> 308
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 Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
 20 25 30
 Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
 35 40 45
 Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
 50 55 60
 Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
 65 70 75
 Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
 80 85 90
 Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
 95 100 105
 Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
 110 115 120
 Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
 125 130 135
 Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

	140	145	150
Val Ser Gly Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met Ser		
155	160	165	
Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln Ala		
170	175	180	
Thr Val Ser Pro Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser Glu		
185	190	195	
Ser Glu Lys Thr Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys Ala		
200	205	210	
Ala Val Arg Ala Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys Lys		
215	220	225	
Lys Lys Ala Pro Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp Ser		
230	235	240	
Asp Gly Ala Lys Pro Glu Pro Val Ala	Met Ala Arg Ser Ala Ser		
245	250	255	
Ser Ser Ser Ser Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser Val		
260	265	270	
Lys Lys Pro Pro Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu Pro		
275	280	285	
Lys Pro Arg Gly Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser Ser		
290	295	300	
Ser Ser Ser Asp Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser Glu		
305	310	315	
Trp Lys Arg Arg Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala Arg		
320	325	330	
Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln		
335	340	345	
Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly		
350	355	360	
Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg		
365	370	375	
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly		
380	385	390	
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu		
395	400	405	
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser		
410	415	420	
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg		
425	430	435	

Leu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	440	445	450	
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	455	460	465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	470	475	480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	485	490	495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	500	505	510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	515	520	525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	530	535	540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	545	550	555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	560	565	570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	575	580	585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	590	595	600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	605	610	615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	620	625	630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	635	640	645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	650	655	660
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					665	670	

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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cagactcaat aattatatta aattaacacc atttgaaaga gaacattggt 100

ttttctga atgctaataa ggalqaaqa ettaaaqca gaagccaada 150
 ccttaccctt ttccctgctt tgatgatget aagcatgacc atgttgttfc 200
 tttcttccac tggcaactttg aagcaaaaata ttccaagact caagctaacc 250
 ttttaagact tgetgcttfc aatagctgt attccctttt tgggttcate 300
 tgaatgaactg gattttcaaa ctcttctctt agatgaggaa agaggcaggo 350
 tctctttggg agccaaagac cacatcttfc tactcagtet ggttgaetta 400
 aacuaaaatt ttaagaagat ttattggcct gctgcaaaag aacgggtgga 450
 attatgtana ttagctggga aagatgccaa tacagaatgt gcaaatttca 500
 tcagagtaet tcagccctat acaaaaactc acatataatgt gtatggaact 550
 ggaqcatttc atccaatatg tgggtataat gctcttggag tctacaagga 600
 ggaatattata ttcaaaactag acacacataa tttggaglet ggcagactga 650
 aatgtccttt cgalccctcag cagccttttg ctccagtaat gacagatgag 700
 tactctact ctggaacagc ttctgalitc ctgggcaag atactgcatt 750
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

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Ile	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120
Glu	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135
Glu	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
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Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
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His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu
				260					265					270
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
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Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
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Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
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Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335					340					345
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
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Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	
				410					415					420	
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	
				425					430					435	
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	
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Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	
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Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	
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Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	
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Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	
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Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	
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Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	
				605					610					615	
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	
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Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	
				635					640					645	
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	
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Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr	

665	670	675
Pro Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu		
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Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu		
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu		
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Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp		
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His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp		
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 <213> Artificial

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<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-45
 <223> Synthetic construct.

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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

	305		310		315									
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly
				320					325					330
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro
				335					340					345
Asp	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala
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Pro	Asp	Pro	Gly	His	Pro	Asp	Pro	Leu	Thr					
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 Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
 65 70 75
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Lys Arg Phe Ala Ser Leu Ser Arg Phe	215	Val Glu Thr Leu Val Val	220		225
Ala Asp Asp Lys Met Ala Ala Phe His	230	Gly Ala Gly Leu Lys Arg	235		240
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Phe Thr Arg Gln Asp Leu Cys Gly Val	320	Ser Thr Cys Asp Thr Leu	325		330
Gly Met Ala Asp Val Gly Thr Val Cys	335	Asp Pro Ala Arg Ser Cys	340		345
Ala Ile Val Glu Asp Asp Gly Leu Gln	350	Ser Ala Phe Thr Ala Ala	355		360
His Glu Leu Gly His Val Phe Asn Met	365	Leu His Asp Asn Ser Lys	370		375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	380	Ser Thr Ser Arg His Val	385		390
Met Ala Pro Val Met Ala His Val Asp	395	Pro Glu Glu Pro Trp Ser	400		405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	410	Phe Leu Asp Asn Gly Tyr	415		420
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<210> 320

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<211> 1174

<212> DNA

<213> Homo sapiens

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 gaaggaaatg aaaaaataat tcttttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaaglacaa attccatgaa aagctcacac ctgtaatect 1800
 agcactttgg gaggtgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagcctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctqlagtccc agcattccgg 1950
 gaggtgagg tgggaggatc acttgagccc agggaggttg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaanata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

80					85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
			95						100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
			110						115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
			125						130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
			140						145					150
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
			155						160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
			170						175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
			185						190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
			200						205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
			215						220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
			230						235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
			245						250					255
Ser	Lys	His	Asp	Tyr	Val									
			260											

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aacctgctt caaagcagaa 50
 gtacagttc cggagtcacg ctggctaaaa ctcatccag aggataatgg 100
 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaaatg 150
 gtgggcacag tggtgtcac tgtcatgctt cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcac aatctatgat 300
 tccctgctgg ctcttctctc ggacctacag gcagccagag gactgatgtg 350

tucgcttcc gtagtgctt telltgcttt catgatggcc atccttgcca 400
 tgaatgcac caggtgcacg ggggacaatg agaaggtgaa ggtcacatt 450
 ctgtgaagg ctggaatcat ctccatcatc acgggcatgg tgggtctcat 500
 cctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 taagtgaatgt tgcacaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttggg ggagctctgt totgtctggt 650
 tttttgttg aacgaaaaga gcagttagct cagatactcg atacctccc 700
 atgcacaaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagtttgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggacc 850
 caaagaaact ttgatttact gttcttaact gcctaattct aattacagga 900
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacc aalgctttga ttgttctaga aagtatagta atttgtttc 1000
 taaggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgta acatttatat ctccataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcctttcag ggaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcttc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaatcc taacttcttt 1400
 atcctcttct cccagaggct ttttttct tgtgtattaa attaacattt 1450
 ttaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaaga aaaagtgatg 1550
 gttttaggaa agtgaataa tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgaaa ctccacctgc tctatgtgg gtacctgagt caaaattgtc 1800

atttttgttgc tctgaaaaat aaatttcctt cttgtaccat ttctgtttta 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tttttgtgac aatccaattt gaaagtttgt gtcgacgtct gtcctagctta 1950
 atggaatgtg ttctatttgc ttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 ctgggctggg tgaatggcct ggtctctgtt gccctgccca tgtggaaggt 100
 gaccgcttcc atcgccaaca gcctcgtggt gccccagggtg gtgtgggagg 150
 gccgtgggat gtcttcgctg gtgcagagca ccggccagat gcagtgcacg 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atgcccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaagcc 350
 cgcctggtgc tcacctctgg gattgtcttt gtcctctcag gggctctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggltgctgtg 550
 ctgcacttgc cctcggggg ggteccaggg cccagccat tacatggccc 600
 gctactcaac atctgccct gccatctctc gggggccctc tgagtacct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcacaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gctctctgtc atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc accttggat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttgaagc cagtcaagct atggaactaa 950
 tgccgaggct gcttgctgtg ctggcttttc aacaagacag actgtcccca 1000
 agagttcctg ctgctgctgg gggtgggct tccctagatg tcaactggaca 1050
 gctgcccccc atctactca ggtctctgga gctctctct tcaccttg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgttcc ctccgtctg ataagacgtc cccccccag ggccaggctcc 1200
 cagctatgta gacccccgc cccacctcga acactgcacc cttctgcct 1250

gagcctctg tctcaccccc tttaactcca catttttata aaataaagca 1300

tttttgita gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
			35						40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
			50						55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
			65						70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
			80						85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
			95						100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
			110						115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
			125						130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
			140						145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
			155						160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
			170						175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
			185						190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
			200						205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
			215						220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

331
gccaaggaga acatcatcaa agactttctt agactcaaaa ggtttccacg 50
tt tacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttcccttggc atggtgggga ctcttccac aacctttctg cctcagtggt 200
agagtatcag cttttgttgg cagcaacatt attgtctttg agaggetctg 250
ggaagggtct tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggtctctc cgcctgccct ggaacagcc 350
cgggcccctca tgtgtgtggc tgttgetctc tcttggatcg cctgtctat 400
tggcatctgt ggcataaagg aggtccagtg cacaggtctt aacgagaggg 450
ccaaagcata ccttctggga acttcaggag tctctttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acatagggtca gaaacgagag ctgggagcag 600
cacttttctt tggctgggca agcgtgctg tctctttcat tggaggggggt 650
ctgctttgtg gattttgtct ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg totaatgcct ccttttggct 800
ccaagtatgg actatggtca atgttttcta taaagtcttg ctgaaaactg 850
taagtatgtg aggcaggaga acttgcctta tgtctagatt tacattgata 900
cgaaagtctc aatttgctac tgggtggtagg aatgaaaatg acttacttgg 950
acattctgac ttcagggtga ttaaattgat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtatacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

	5	10	15
Arg Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc aqcatttaca 150
 agaagtatcc agtggtgccc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tottcaogat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggcctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgcgcga tggtgcctc cccgcgcgg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccitggcag cctgaagcgc cagaagcggc agctgtggga cggactcgg 300

cccaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550

agcgattctc ttcattgtatc tccaatgccc tiacaactact tggttttctga 600

tttctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 ttgaggttaa aacaacacat qtaaatgcct tttgataatt catgggaatg 700
 tttt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<207> 336
 <210> 148
 <211> FRT
 <212> Homo sapiens

<400> 336
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
 1 5 10 15
 Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
 cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
 agccgggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgacctgat 100
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgaggggcggg 200
 gacccaactgc ccagccgtc agggacccca acgccatccc agcccagcgc 250

...aggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 ...agcct gagacacaga ggtcaagctg cacagccaga gcccacacg 350
 ...acag caacacggcc agcccggac tcccgcagg agccctcgt 400
 ...aggtg aaattcctca atgattcaga gcaggtggcc agggcctggc 450
 ...acac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 ...aggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 ...taggc agccttcacc tccctccaa ctgcgttctc cactgccacg 600
 ...acagag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 ...ggccctt ccgggtgga aatcggcagc ctgctgctgc cctgctgct 700
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 ...agcgtgccg gccctcccg accttgctcc ccgcgcccg ggggagctg 900
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 ...gccagcct gcgcgcaga ggactcccg gactggcgga ggccccgcc 1000
 ...tgccaccgc ggggtccgg gccacctccc ggggtgctg aacctcagcc 1050
 ...cgactggga gtgggtcct cggggtcgg catctgctgt cgtgcctcg 1100
 ...gccccggga gaggcgggc gccccgggg ccggtcttag tgttctgcc 1150
 ...gaggaccag ccgcctcaa tccctgacag ctccctgggc tgagttggg 1200
 ...acgccaggtc ggtgggaggc tgggaaggg gagggggag gggcagagga 1250
 ...gttccccga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5				10					15	
Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
			20					25					30	
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
			35					40					45	

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Leu	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgccctctcc agattcccca ggcctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150

atgacaaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

atggga tgggtttgag gggtactccc tgagtgaactg gctgtgcctg 300
 gttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tttttttt gactatggcc ttttccagat caacagccac tactggtgca 400
 ttttataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
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 gtttggagca cgggggatga acaactgggt agaattggagg ttgcaactgtt 550
 caggccggcc actctcctac ttgctgacag gatgccgctt gagatgaaac 600
 aaggtgctgg tgcaccgttg agtcattcca agactcctgt cctcactcag 650
 ggatttttca ttttttcttc ctactgcctc cacttcatgt tattttcttc 700
 ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
 tcttggttcc ctcttactc ccatctggac ccagtcacct ggttctgtc 800
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala	1	5	10	15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val	20	25	30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser	35	40	45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser	50	55	60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe	65	70	75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser	80	85	90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn	95	100	105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala	110	115	120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly	125	130	135	
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg						

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ctctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc ttctcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 345

agcttcttg ccttaaata ggcagctc atcagtcgt gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

tctgacctga ctggaagcgt ccaaagaggg acggtgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatt tttttttccc 150
aaggagaaaa cggggglaaa gggagggag caattcaatt tgaagtcct 200
gtgaatgggc ttccagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagt gaagcaggtc 300
ttgcacacgc tgttggcaaa tgcaggacc aggttaagt actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgcaa 450
gttctagcaa catgtccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650
tcccaggatt gggtaactga agctgaggat gagggtgaag agtacagccc 700
tctggagggc ctgccaccct ttatctcaact ggggaggat cagctgctgg 750
tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800
ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900
aggagttgac cccgttcagc ctggaacccac gtggcctcca ggaggcactc 950
agtgcctgca tccccctcca gagggtcttg cccgaggtgc ggcacccact 1000
gtgtctgcag cagcaccctc aggcagcct gccacagcc agcgtcatcc 1050
tctgtttcca tgatgaggcc tggctcactc tctgaggac tgtacacagc 1100

caa cagtgccacg ggccttcctg aaggagatca tccctcgtgga 1150
 caagc cagcaaggac aactcaagtc tgetctcagc gaatatgtgg 1200
 caagc gaa gggggtgaag ttactcagaa gcaacaagaq gctgggtgac 1250
 caagc cagc ggatcctggg ggcacacaga gccacccggg atgtgctcgt 1300
 caagc cagat gcccaatgag agtgcacccc aggetggetg gacccctcc 1350
 caagc caaat agctggtgac aggagccgag tggatatctc ggtgatagat 1400
 caagc caat ggaagacttt ccagtattac cctcaaaagg acctgcagcg 1450
 caagc caat gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
 caagc caat ggcctccag tccccataa gccccatcag gacccctgtg 1550
 caagc caat aggtggtggc catggacaga cattacttcc aaaacaactg 1600
 caagc caat tctcttatgt cgetgcgagc tggtagaaac ctgcgaactgt 1650
 caagc caat ctgtctctgt ggtggctctg ttgaaatcct tccctgctct 1700
 caagc caat acatctacca aaatcaggat tcccatcccc cctctgacca 1750
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 caagc caat aacctctac aagcatagcc cagaggcctt ctcttgagc 1850
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 caagc caat ggggtgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
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 caagc caat ctgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050
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 caagc caat atatatctca tgaagctgat ccttttgtgt gtgtgctcct tgtgttagga 2500
 caagc caat gacaaaaaag ctctatgaaa gaatatagga agtttctcct ttccacacct 2550

catctcattg actgctggct gctta 2575

4210 347

4211 639

4212 PRT

4213 Homo sapiens

4400 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu Val	Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
	Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val				
	560		565		570
Ile	Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln				
	575		580		585
Ile	Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser				
	590		595		600
Gly	Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu				
	605		610		615
Tyr	Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe				
	620		625		630
Asp	Gln Ile Asn Ala Val Asp Glu Arg				
	635				

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgtg cgaggtggtg aaaacctga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
 cggcaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
 ctacagacatg gagtcacagga tgtggcctgc gctgctgctg tcccacctcc 100
 tccctctctg gccactgctg ttgttgcccc tcccaccgcc tgcacagggc 150
 tcttcactct cccctcgaa cccaccagcc ccagcccgcc ccccggtgtg 200
 caggggaggg cctcggccc cactgcatgt gtgcgtgtgg gagecagcac 250
 ctccaccaag ccgactcctt cgggtcccaa gatcagctcg gcaagtcctg 300
 cctggcactg cccccccagc ccccccatca ggttttgagg aggggcggcc 350
 ctcatcccaa taccctggg ctatcgtgtg gggccccacc gtgtctcgag 400
 aggatggagg ggaccccaac tctgccaatc ccggatttct ggaactatgt 450
 tttgcagccc ctcatgggct cgcaccccca ccccccaact caactccat 500
 gcgaggtgat ggagatgggc ttatccttgg agaggcaact gccaccctgc 550
 ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
 gtcacaatta ccactccat catcattgtt ctgctggcca ctggcactat 650
 cttcaagtic tgtcgggacc gcagccagaa gcgacgcaga cctcagggc 700
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 caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850
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 tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
 tgggggtgcc ctctggatgg gtatgagga ggcaggcgtg gcctccaca 1000
 gccctggcc ctcccaaggg ggttgacca gtcctctctt gggaggcacc 1050
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 tctgacagat gggttttgg gagtcgctg ctgcactaca tgagaaagg 2050
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 aagtctacc ttccttccc ggaacctc ctgtccctc atttctccc 2300
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 ttctgtgtt gatcatctg aattactgt ggalgtaagt ttcaaaattt 2500
 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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Ile	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
				20				25					30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35				40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50				55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65				70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80				85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95				100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110				115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125				130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140				145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155				160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170				175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185				190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200				205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215				220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230				235					240	

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgggtcccg ccgcccgtg cctcactcc 50

cggccaggat ggcatactgt ctggccctgc gcattggcgt gctgctggtc 100

tccqgggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgcccgcg ggagaaggcc 200
 ccctggaagag caccagcccc ggcggggagc ccgtggacac cggccccca 250
 acccccacgc tgcgccagg acccgaggac agcaccgcgc aggagcgget 300
 agaccagggc ggcgggtgc tggggcccg cgtatcgcg gccatcgtga 350
 tgcgcgcct gctggccacc tgcgtggtgc tggcgcctgt ggtcgtcgcg 400
 ctgagaaagt tttctgctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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 ctgcgggatg tgattaaagt cctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
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 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
 125 130 135
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

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				20				25						30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35				40						45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50				55						60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65				70						75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80				85						90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95				100						105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110				115						120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125				130						135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140				145						150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155				160						165
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170				175						180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185				190						195

Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
		200					205					210
Leu	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala
		215						220				225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala
		230						235				240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu
		245						250				255
Leu	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr
		260						265				270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

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NA
Artificial

<211> Artificial Sequence

<212> 1-50

<223> Synthetic construct.

<400> 362

atctccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363

<211> 1777

<212> DNA

<213> Homo sapiens

<400> 363

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cctcagcggg gacccgggct cagggacgcg gcggcgggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggctcgt gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggccgggttga cctcagtcct ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
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 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
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 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
		110					115					120
Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
		125					130					135
Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
		140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe
		155							160			165
Thr	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu
		170						175				180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg
		185							190			195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser
		200							205			210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr
		215							220			225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro
		230							235			240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp
		245							250			255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys
		260							265			

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
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 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

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 aagtcaaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
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 catgtttata aagtaaaaaa a 1321

<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366
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 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala		95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp		110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly		125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn		140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile		155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala		170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu		185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr		200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys		215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys		230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys		245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu		260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn		275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn		290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe		305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu		320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp		335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val		350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg				365	370	

<210> 367

<210> 367
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
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<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggttt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
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 ctggggcaac cgggttgcct ctgctcttgc tgatggcggt aacagcgccc 150
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 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
 gccaccaca gccccagycg ctgagacggc ggccttcatt gaacgccttg 700
 agatggaaca ggcccagaag gcccaagaacc cccaggagca gaagtccttc 750
 ttgcgcaaat actggatgta catcattccc gtcttccgtg tctcatgat 800
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 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaatc actgctcact tgatacgtta ttcaqaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcaactgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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cagcaggtcg tccgggggcc caccatgctg gtgaactgctt accttgcctt 150

tgtaggcctc ctggcctcct gctgggggt ggaactgtca agatgcggg 200

tttttttt tggaaagggc tgcagcaatc cctccttctt tgggtttcaa 250
 ttgtttct atcaggtcta cttcctggcc ctggcagctg attggtttca 300
 tttttctac ctctataaac tctaccagca ttaactactt ctggaaggtc 350
 aaattgcaat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
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 cctctttctc ctgacttact cactatgctg ctttaacaaa ctctctcaag 500
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
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 tctggaacca tgtgtggct gtagtggcag gtgtggcagc tgaggtgta 700
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 ctgcttggct cttccctgta ccgtatgcc acctccaaga ggtaccacct 1050
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 tcttcatgtt gaatttctct accagcccag gccaggagag tccggtggag 1150
 tcttcatag cctttctact tattgagttg gcttgtggat tatacttctc 1200
 cagcatgagc ttctacgga gaaagggtgat cctgagaca ggcaggtctg 1250
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 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggaat gatgggggtg atggactgga aagaagggtc caaaagtctc 1650

Leu Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

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gccctggaga tggccccggc cgccgcgggc tgggtgttgc tegtgtctgt 100
gtccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaaag actttggtgg tatctttcac acaaggtatg agcagattca 250

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ccttctccccc gctgaaccctc cagaggccctg cgggggaactc agcaaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctctccttc 350
 ctctcaga ctccgggtgt ccaggagcac ggccggccgg ccgtgatcat 400
 ctctcacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagttacca ggcacacgt gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccggcg ctctctggaa cagcatgggc tgccatgggc 550
 cactcatttc atcccagtc atgtaccag catccccacc tttgagctgc 600
 tqcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgaat ctgagctggg aaggggaaac ccaggaattt tgetacttgg 700
 aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcgtt gctaggtga aagggagccc acaccactgg ccttcccttc 800
 cccagggccc ccaaggtgt ctcatgtac aagaagaggg aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcttgagagc catctgtgac ctgtcacact cacttgctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20						25					30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35						40					45

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
			50						55					60

Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
			65						70					75

Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
			80						85					90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
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 ggctggtggt gatggtctgt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgaactggg aaaatgcccc tctctctcta 150
 ctggccctac ggetgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgtctgc cagacccatg actgctgcta tgaccacctg 250
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35					40						45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50					55						60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65					70						75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80					85						90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95					100						105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110					115						

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatqccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50

agcgatgtgg aggggtgccg gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgc 150

ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggetgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttggg 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

cacctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggcca gatctcctct gcctacccca gccaaaggag 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggcct tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650

ggtatggggc catccgagct gaggccatct gtgtgggtgt ggcctgatgt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
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 atacagatgt ggcagctcag gtagccccc aaattgctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgaggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttcttggg 400
 tgtcagcgag cctgactca ctacagtgcg gctgacaggg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg gggttcaatg taattaggct actgagcgga tcagctgtag 550
 cactgggtat agccccact gtcttactga caatgcttct tctgcccga 600
 cgaggtatgc ctaagggctg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatatctgct ggttgcttag 700
 gtttgtccct tcgtataaac agccttcaaa aacttaagta taatcaattt 750
 aaagggtctc accagctcac ctggctatac ctgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagaetc aaagagctga 850
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 aacctggaac ttttgacctt gggatataac cggatccgaa gtttagccag 1100
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 aatgcagcag aatatattgc tccctgttaa actggctgaa aagttttaaa 1500
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 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
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 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggacctgc acctataaca aatcgggctc cagggagtgat gaqgtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtgcttta 2100

tttttcttg gtgactatca agggaaacgg atgccccccc tccccctccc 2150
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 tttttcttc ggtcatttct cttcctatca taatcaaccc attgaaattt 2250
 tttttcttc atcaatgiga agcttgaact ccggtttaat ataataccta 2300
 tttttcttc ccctttactg attccattaa tctgcattt gttttaagat 2350
 tttttcttc tcataggtaa aaaaaaaaaa 2379

<212> 385

<213> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

200	205	210
Phe Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	
215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys	
230	235	240
Phe Ser Val Ile Gly Gln Thr Met Ser Trp	Thr Trp Ser Ser Leu	
245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile	Glu Ala Phe Ser Gly	
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn Leu	Gln Arg Leu Asn Leu	
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln	Glu Ile Leu Asp Ser	
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala	Gly Asn Ile Trp Glu	
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn	Trp Leu Lys Ser Phe	
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys	Ala Ser Pro Lys Glu	
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala Val	Lys Asn Tyr Ser Ile	
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp	Leu Ala Arg Ala Leu	
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro	Arg Pro Lys His Glu	
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly	Ala Thr Glu Pro Gly	
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile	Ser Phe His Lys Ile	
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser	Val Leu Val Ile Leu	
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr	Pro Ala Ser Met Lys	
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg	His Arg Lys Lys Lys	
455	460	465
Arg Gln Ser Leu Lys Gln Met Thr Pro Ser	Thr Gln Glu Phe Tyr	
470	475	480
Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr	Ser Glu Met Leu Leu	
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtecccagg acatgggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgaqtta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaataatg tcaagatcca gaacttttcag tgtaacctca 100
 gccatctcaa ccatagggat ctgtgtgttg ccgatattcc agttgggtgt 150
 ctccgacctc ccattgcgaag aagatgaaat gtgtgttaaata tataatgacc 200

...metaa tggctggat atctggatcc tectgtcgt ggttttggg 250
 ...gcttctc tctgtggagc tgtggtcctc tgcctccagt gctggtgag 300
 ...tggga attgattctc acagggcac catggcagtt tttgtgttg 350
 ...tggga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
 ...tccacc ttcaaaactca aacccctgac ctatatcctg ttectgctc 450
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 ...ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr

1

5

10

15

Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp		
		20					25					30		
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
		35						40					45	
Leu	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Val	Leu	
		50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
		65						70					75	
Pro	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
		80						85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
		95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro
		110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser
		125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr				
		140						145						

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtg tcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

Artificial Sequence
 1-47
 Synthetic construct.

490-393
 ccagttgggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

100-394
 2340
 DNA
 Homo sapiens

100-394
 gacgcgagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
 acccaccggc gttctctcag ctcgatcttg aggcctgttc gccagtggtg 100
 gacgcagctg acgcctcgtt attagctctc gctgcgtcgc ccgggtcag 150
 aagctccgtg gggcgggcga ccgtgacgag aagcccacgg ccagctcagt 200
 tctctctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
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 ctctgtgaag atgaagaata tacaatattg aggatatltt tttctttttt 350
 ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
 gctctgttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
 tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatittgg 500
 gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
 tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650
 tggcaggata tgggatctg aaaagaacaa ttgctgtcct tctggatgac 700
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 catgtagcaa taattacaat attttattaa aataaataig tgaaatattg 2250
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 acctttatgt gaagaaatta atttatatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	

Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu	
			20					25					30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
			35						40					45
Asp	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
			50						55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
			65						70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
			80						85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
			95						100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
			110						115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
			125						130					135
Ser	Gly	Ser	Ile	Arg										
			140											

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
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 tccagcccc accatgcgt gcccccgt getgetgctq gccgtgagtq 100
 gggcccagac aacccqcca tgcctccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat cctctggac acagcccact 250
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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu
				20				25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys
				35				40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
				50				55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn
				65				70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu
				80				85					90
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe
				95				100					105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly
				110				115					120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser
				125				130					135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser
				140				145					150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly Pro Thr Ile Leu	350		

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

gatttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga agggtgagct acgttggctt totggaagg 100
gaggetatat gcgtcaattc cccaaaacaa gttttgacat ttccctgaa 150
atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200
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tgetgcctcc tgcgccattt gctaagactc tatctggaca gggattttaa 650
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 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
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 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
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 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20						25				30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35						40				45	
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
			50						55				60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65						70				75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80						85				90	

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<209> 404
a cccctt aagattctga tgtcaa 26

<210> 405
<211> 323
<212> DNA
<213> Homo sapiens

<214> 405
ccgctatcgt cttgcgctac tgcctgaatgt ccgtcccggg ggaggaggag 50
aggctttttgc cgcctgaccca gagatggccc cgagcgagca aattcctact 100
ctccgggtgc gggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgcctcggtt 200
ggagacgggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccggccat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aatcagtc tggagggat gatggctggf gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattggaa 500
ggaaaaagga aactggaagg aaaaccattg cgaatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga aactacttg gtattgaata caccacttga 700
ggacaatata atgactcacg gtttatcaag ttatggtct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgccttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgaccc cttgggtcaat ggtgttcttg 950
cttacttatg aaaaaatcag agagatgagt ggaatcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgccgacatccc qttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcqqaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcggggac gccggcaggg ttgtggcgca gcagtclect 50
tcttgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatth atgcttaaga agtaaaaaatg gcaggcttcc 150
tagataatth tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250
qtggataatg attgatgcag ctgtgggtgta tccaaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtattht ccacattggc thttttcatg 350
ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400
ctgtthlagga agaacaggtg ctcgagtttg gctthttcatt ggtthttcatgt 450
tgatgtthtg gtcacttatt gcttccatgt ggattcttht tgggtgcatat 500
gttaccnaaa atactgatgt ttatccggga ctagctgtgt thtttcaaaa 550

380

ttttttagca ctctgatcta caaatitgga agaaccgaag 600
 ctgagatcac ttcttaagtc acattttcct ttgttatat 650
 gta gataggtttt ttatctctca gtacacattg ccaaatggag 700
 attgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttcttagt ttatgaaat ttctttattt ttcaattgcat agactgttaa 800
 tatgatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tttcttgag atttagaact tgatctactc cctgagccag gggtacatca 900
 tttgttcatt ttagaagtaa ccactcttgt ctctctggct gggcacgggtg 950
 gctcatgctt gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggtgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgagct gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgattttc 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtt aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25				30	
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40				45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55				60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70				75	

P	r	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
					80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
 atggcaggct tcttagataa ttttcgttgg ccagaatgtg 40

<210> 414

8271 1337
 NA
 213 homo sapiens

114
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 qcagctggcc cactgggggc ccgcaanact ccgtctcacc ctctggggcc 100
 actgcattcta qaggagggcc gtctgtgagg ccactacccc tccagcaact 150
 qqaaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
 gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
 aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
 acctggacag gatgagagtg tcaggtgtgc ttgcctctct ggccctcacc 350
 tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
 catgaaaacc atccgtctgc cagctggctt ggcagcctcg cccaccaagg 450
 agatccaggt taaaaagtac aagtgtggcc tcattcaagcc ctgcccagcc 500
 aactactttg cgtttaaaaa ctgcagtggg gccgccaacg tcgtggggcc 550
 tactatgtgc ttggaagacc gcatgatcat gagtctgtg aaaaacaatg 600
 tgggcagagg cctaaacatc gccctgggtg atggaaccac gggagctgtg 650
 ctgggacaga aggcatttga catgtactct ggagatgta tgcacctagt 700
 gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctctt 750
 acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800
 gacttgggga gtacctacgc aaaacaactg ggcttccggg acagctgggt 850
 ctccatagga gccaaagacc tcaggggtaa aagccccctt gagcagttct 900
 taaagaacag ccagacaca aacaaatagc agggatggcc agagctgctg 950
 gagatggagg gctgcatgcc ccgaagcca ttttaggggtg gctgtggctc 1000
 ttctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
 cccqgcaggg gctgaggaag aggagcaggg ggtgctgcgt ggaagggtgt 1100
 gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaaccc 1150
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 accagctgtc tgtggagaga atgggggtgt ttcgtcaggg actgctgacg 1250
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 tatttttgct ggttttqaaa aaaaaaaaaa aaaaaaa 1337

414
4
Homo sapiens

<400> 415

1	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	
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	Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe
					20					25				30
	Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro
					35					40				45
	Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys
					50					55				60
	Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala
					65					70				75
	Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile
					80					85				90
	Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala
					95					100				105
	Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe
					110					115				120
	Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys
					125					130				135
	Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp
					140					145				150
	Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp
					155					160				165
	Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp
					170					175				180
	Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu
					185					190				195
	Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp
					200					205				210
	Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe
					215					220				

<210> 416

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<210> 1-21
 <211> Synthetic construct.

 <400> 416
 agtca cgacatggat g 21

 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 417
 ggatggccaq aactgctg 18

 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 418
 aaagtacaag tgtggcctca tcaagc 26

 <210> 419
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 419
 tctgactcct aagtcaggca ggag 24

 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 420
 attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggccctcatca agccctgccc agccaactac ttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtctctggg atccagaaac ccattgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
caagccagga gctcgctcgc tctctctctc tctctctcac tctctcctcc 200
ctctctctct gctgtctcta gtctcttagt cctcaaattc ccagtcacct 250
gcaccccttc ctgggacact atgttgttct ccgcccctct gctggagggtg 300
atttggaacc tggctgcaga tgggggtcaa cactggacgt atgaggggcc 350
acatggtcag gaccattggc cagcctctta ccttgagtgt ggaaacaatg 400
cccagtcgcc catcgatatl cagacagaca gtgtgacatt tgacctgat 450
ttgctctctc tgcagcccca cggatatgac cagcctggca ccgagccctt 500
ggacctgcac aacaatggcc acacagtgca actctctctg cctctaccc 550
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atgacagctt gagtgaagct gctgagaggc ctcagggcct ggtgtctctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgaqtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

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 catgcatgtg gatgaattcc ctctatgcc atcaggaagc ctctaaaatg 1350
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 ccttccctg gacatctctt agagaggaat ggaccacggc tgtcattcca 1450
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 gaaatcgtg tgttgttaat gcagagacca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
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 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

	80	85	90
Pro Ser Thr Leu Tyr	Leu Gly Gly Leu	Pro Arg Lys Tyr Val	Ala
	95	100	105
Ala Gln Leu His	Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly	
	110	115	120
Pro Glu His Gln	Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
	125	130	135
Ile Val His Tyr	Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala	
	140	145	150
Ala Glu Arg Pro	Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
	155	160	165
Val Gly Glu Thr	Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
	170	175	180
Leu His Glu Val	Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
	185	190	195
Phe Asn Leu Arg	Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
	200	205	210
Arg Tyr Asn Gly	Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
	215	220	225
Leu Trp Thr Val	Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
	230	235	240
Leu Glu Lys Leu	Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
	245	250	255
Ser Lys Leu Leu	Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
	260	265	270
Gln Arg Met Val	Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
	275	280	285
Thr Thr Gly Glu	Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
	290	295	300
Cys Leu Cys Leu	Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
	305	310	315
Arg Lys Lys Arg	Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
	320	325	330
Ala Gln Ala Thr	Thr Glu Ala		
	335		

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 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
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<210> 427
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<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

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tttttt gggactccct cccacaaaac tggctccgga tcaagggaaca 200
 ctacccaaacc aacagcagtc aaatcaggtc ttcccttctt taagtctgat 250
 ctcccaaca cagatgctca cactggggcc agatctgcat ctgttaaate 300
 cctgtgagg aatgacacct ggtaccaga cccaccatt gacctggga 350
 tggtttatg tacaacagca actgcacca catgtgttac caattttgt 400
 ctacaaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aatcttcac gagccctac atccattcct tgttccggg aggcacctg 500
 cctccagtc aggcagggc taatccagat gtccaggatg gaagccttc 550
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 gcttcccaac tccagtggc acagatgacg actttgcagt gaccacccct 650
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 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatatc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 ctittaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgtgctt ggatgatatg catattaaaa catatttggg aaactggaaa 1000
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 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
				20				25						30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
				35				40						45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50				55						60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65				70						75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
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<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgcgcg ctccccgcag cggctccggg gcttctgtgt gctcctgtgt 200
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aaaggcgag ctccggcaga gggagggtgt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgccttgtc gagacgggag cctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
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actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttccgctaaa atgcagaaat gcatgctgtc 600
agcgttggtg ttccacattc aatggagctg aatgttcagg acctcttccc 650

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 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcacatttat 850
 tgaagaacta ccaaaataaa tgctttaatt ttcatctgct acctcttttt 900
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<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35					40					45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50					55					60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65					70					75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80					85					90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95					100					105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110					115					120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125					130					135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Tyr	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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<210> 434
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<220>
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<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
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 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
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 actccaggca ccactgtgtc tccc 24

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<210> 443
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<400> 443
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aaaggacacc gggatgtg 18

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 <400> 449
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 <400> 450
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 <400> 451
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<212> acgtg gcagtgga 18

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<210> 470

<211> 19

<212> DNA

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<400> 470

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<210> 472

<210> 24
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 <400> 476
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1000

artificial oligonucleotide probe

4000

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